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FIG. 1

ATGGCGCCGCCGCCGCCGCCGCTGCTGCCCGTGCTGCTGCTCTGGCCGCCGCCGCCGCCCTGCCGGCGATGGGGCTGCCG
AGCGGCCGCTGGGAGCCGCGCGTACCCGGCGGGACCCGCGCTTCGCCCTCCGGCCCGGGCTGTACCTACGCGGTGGGCG
CCGCTTGCAACCCCGCCGCCGCCGGAGCTGCTGGACGTGGGCGCGATGGGCGGCTGGCAGGACGTGCGCGCGTCTCG
GGCGCGGGCGCCCGCTGCCGCTGCAAGTCCGCTTGCTGCCCCGAGTCCCCCGACGGCGCTGAGCCGCCCGCTGCCGGC
GCGCACGCACCTTCCCGCTGCGGAGCCCGTGCCCGCTCTGCGGAACCGGTGCCCGCTCTGCGGGCGGCTCTGCTTCC
CCGTCCCGCGGCTGCGCGGCCGCGCAGCATTCGGCGCTCGCAGCTCCGACCACCTTACCCGCTGCCGCTGCCCGCG
CGCCCCAGGCCCCGCTGTCCCGGCCGTCCATCTGCCCTGCCCGCGGGCGGCTCGGTCCGCTTGCCTGTGCTGTGCCCTT
GCGGCGCGCGCTGCGCGCTGCGGGTGGGACTGGCGCTGGAGGCCGCCACCGCGGGACGCCCTCCCGCTGCGCATCCC
CATCGCCGCCCTGCCCGCGAATTCGCCGAAGCCCGGGCGGGCGCGCGACGGGCCCGGGCGGGACGAGCGGGCAGA
GGGAGCCTGAAGTTTCCGATGCCCAACTACCAGGTGGCGTGTGTTGAGAACGAACCGCGGGGACCCCTCATCTCCAGCT
GCACCGCTACTACACCATCGAGGGCGAGGAGGCGCGTGAGCTATTACATGGAGGGCTGTTCCAGAGCGCTCCCGG
GCTACTTCCGAATCGACTCTGCCACGGCGCGGTGAGCACGGACAGCGTACTGGACCGGAGACCAGGAGACGCACGTC
CTCAGGGTGAAAGCCGTGGACTACGTACGCGCGCGCTCGGCCACCACCTACATCACTGTCTTGGTCAAAGACACCAA
CGACCACAGCCCGGTCTTCGAGCAGTCGGAGTACCGGAGCGCGTGCGGGAGAACCTGGAGGTGGGCTACGAGGTGCTGA
CCATCCGCGCCAGCGACCGCGACTCGCCCATCAACGCCAACTTGCCTTACCGCGTGTGGGGGGCGCGTGGGACGTCTTC
CAGCTCAAACGAGAGCTCTGGCGTGGTGAGCACCGGGCGGTGCTGGACCGGGAGGAGGCGGGCCGAGTACCAGCTCCTGGT
GGAGGCCAACGACCGAGGGGCGCAATCCGGGCCCGCTCAGTGCCACGGCCACCGTGTACATCGAGGTGGAGGACGAGAACG
ACAACTACCCCCAGTTCAGCGAGCAGAACTACGTGTTCCAGGTGCCCGAGGACGTGGGGCTCAACACGGCTGTGCTGCGA
GTGCGAGGCCACGGACCGGGACCGGGCCAGAACCGGCCCATTCATACAGCATCTTCAGCGGGAACGTGCGCGGCCAGTT
CTACTGCACTCGCTGAGCGGGATCCTGGATGTGATCAACCCCTTGGATTTCGAGGATGTCCAGAAATACTCGCTGAGCA
TTAAGGCCCAGGATGGGGGCGGGCCCCGCTCATCAATCTTCAGGGGTGGTGTCTGTGCGAGGTGCTGGATGTCAACGAC
AACGAGCCTATCTTTGTGAGCAGCCCCCTTCAGGCCACGGTGTGGAGAATGTGCCCTGGGCTACCCCGTGGTGCACAT
TCAGCCGGTGGACCGCGACTCTGGAGAGAACGCCCGGCTGCATATCGCCTGGTGGACACGGCTCCACCTTTCTGGGGG
GCGGCAGCGCTGGGCTAAGAATCTGCCCCACCCCTGACTTCCCTTCCAGATCCACAACAGCTCCGGTTGGATCACA
GTGTGTGCCGAGCTGGACCGGAGGAGGTGGAGCACTACAGCTTCGGGGTGGAGGCGGTGACCCAGGCTCGCCCCCAT
GAGCTCTCCACCAGCGTGTCCATCAGGTGCTGGACGTGAATGACAACGACCCGGTGTTCACGCAGCCACCTACGAGC
TTCGTCTGAATGAGGATGCGGCTGTGGGGAGCAGCGTGTCTGACCTGCGAGGCCCGCGACCGTCAACCCAAACAGTGTGATT
ACCTACCAGCTACAGGGGCAACACCCGGAACCGCTTTGCACTCAGCAGCCAGAGAGGGGGCGGCTCATCACCTGGC
GCTACCTCTGGACTACAAGCAGGAGCAGCAGTACGTGCTGCCCTCACAGCATCCACGGCACACGGTGCACACTGCGC
ATGTCTTAATCAACGTCACTGATGCCAACCCACAGGCCTGTCTTTCAGAGCTCCATTACACAGTGAGTGTCAGTGAG
GACAGGCCTGTGGGCACCTCCATGCTACCTCAGTGCCAACGATGAGGACACAGGAGAGAATGCCCGCATCACCTACGT
GATTCAGGACCCCGTGCCGAGTCCCGATTGACCCCGACAGTGGCACCATGTACCATGATGAGCTGGACTATGAGA

FIG. 1 Continued

ACCAGGTCGCTACACGCTGACCATCATGGCCAGGACAACGGCATCCCGAGAAATCAGACACCACCACCTAGAGATC
 CTCATCTCGATGCCAATGACAATGCACCCAGTTCTGTGGGATTCTTACCAGGGTTCCATCTTTGAGGATGCTCCACC
 CTCGACCAGCATCTCCAGGTCCTGCCACGGACCGGACTCAGOTCCCAATGGCGCTCTGCTGTACACCTTCCAGGGTG
 GGGACGACGGCGATGGGACTTCTACATCGAGCCACGTCCGGTGTGATTCCACCCAGCGCGGCTGCACCGGGAGAAAT
 GTGCCCGTGTACAACCTTTGGGCTCTGGCTGTGGATCGGGGACGTCCACTCCCCTTAGCGCCTCGGTAGAAATCCAGGT
 GACCATCTTGGACATTAATGACAATGCCCCATGTTTGGAGAAGGACGAACTGGAGCTGTTTGTGAGGAGAACAAACCCAG
 TGGGGTGGTGGTGGCAAGATTCGTCTAACGACCTGATGAAGGCCCTAATGCCAGATCATGTATCAGATTGTGGAA
 GGGGACATCGGGCATTTCTTCCAGCTGACCTGCTCAACGGGACCTGCGTGCATGTTGGAGCTGGACTTTGAAGTCCG
 CGGGAGCTATGTGCTGGTGGTGCAGGCCACGTCCGGCTCCGCTGGTGAAGCCAGCCACGGTGCACATCTTCTCGTGGACC
 AGAATGACAACCCGCTGTGCTGCCCGACTTCCAGATCTCTTCAACAATATGTACCAACAAGTCCAACAGTTTCCCC
 ACCGGCTGTATCGGTGTCATCCCGGCCATGACCCGACGTGTGAGACAGCTCAACTACACCTTCTGTCAGGGGCAACGA
 CCTGCCCTGTTGCTGTGACCCGCCACGGGCGAAGTGCAGTGCAGCCGACCTGGACAACAACCGGCCGCTGGAGG
 CGCTCATGGAGGTGTCTGTGCTGTATGGCATCCACACGCTCAGCGCTTCTGACCCCTGCGTGTCAACATCATCGGAC
 GACATCTGACCAACAGCATCACTGTCCCTTGGAGAATGTCCAGGAGAGTTCTGTCTCCCGCTGCTGGCCCTCTT
 CGTGGAGGGGGTGGCCGCCGCTGTCTCCACCACCAAGGACGACGTCTTCTGCTTCAACGTCCAGAACGACCCGACGTCA
 GCTCCAACATCTGAACGTGACCTTCTCGGCGCTGCTGCTGGCGGCTCCGCGGCCAGTTCTTCCGCTCGGAGGACCTG
 CAGGAGCAGATCTACCTGAATCGGACGCTGTGACCAACATCTCCACGACGCGGTGCTGCCCTTCGACGACAACATCTG
 CCTGCCGAGCCCTGCGAGAACTACATGAAGTCCGTGCTGCTGCGATTGACAGCTCCGCGCCCTTCTCAGCTCCA
 CCACCGTCTTCTCCGCCCATCCACCCCATCAACCGGCTGCGCTGCGCTGCCGCCCGGCTTCAACCGCGACTACTCC
 GAGACGGAGATCGACCTCTGCTACTCCGACCCGCTGCGGCCAACCGCCGCTGCCGACGCGGAGGGCGGCTACACCTG
 CGAGTCTTTCGAGGACTTCACTGGAGAGCAGTGTGAGGTGGATGCCCGCTCAGGCCGCTGTGCCAACGGGGTGTGAAGA
 ACGGGGGACCTGCGTGAACCTGCTCATCGGGGCTTCCACTGCGGTGTCTCTCTGCGCAGTATGAGAGGCCCTACTGT
 GAGGTGACCAACAGGAGCTTCCGCCCAAGTCTCTGTCACCTTCCGGGGCTGAGACAGCGCTTCCACTTACCATCTC
 CCTACGTTTGGCACTCAGCAAAACCAACGGCTTGTCTCTACAACGGCGCTTCAATGAGAAGCAGACTTCACTGCCCC
 TGGAGATCGTGGACGAGCAGGTGCAGCTCACCTTCTCTGACGGCGAGACAACAACGACCGTGGCACCAAGGTTCCCA
 GGTGTGAGTGACGGCGGTGGCACTCTGTGACGTTGAGTACTACAACAAGCCCAATATTGGCCACCTGGGGCTGCCCA
 TGGGGCGTCCGGGAAAAGATGGCGGTGGTACAGTGGATGATTGTGACACAACCATGGCTGTGCGCTTTGGAAGGACA
 TCGGGAATACAGCTGCGCTGCCAGGGCACTCAGACCGGCTCAAGAAGTCCCTGGAATCTGACCGCCCTTACTCCTG
 GGGGTGTCCCCAACCTGCCAGAAGACTTCCAGTGCACAACCGGCAGTTCTGTTGGCTGCATGCCGAACCTGTGAGTGA
 CGGCAAAAATGTGGACATGGCCGATTCATCGCAACCAATGCCACCGGGAAGGCTGCGCTGCTCGGAGGAACCTTCTGCG
 ATGGGAGGCGGTGTCAGAATGGAGGCACCTGTGTCAACAGGTGGATATGTATCTGTGTGAGTGTCCACTCCGATTGCGG
 GGAAGAATGTGAGCAAGCCATGCCCTACCCCGAGCTCTTCAAGCGGTGAGAGCGTCTGTCTTGGAGTGACCTGAACAT
 CATCATCTCTGTGCCCTGTTACCTGGGGCTCATGTTCCGGACCGGGAAGGAGGACAGCGTTCTGATGGAGGCCACCACTG
 GTGGGCCACCACTTCTCGCTCCAGATCTCTGAACAATACCTTCCAGTTTGAAGGTGTCCACCGCCCTTCCGATGTGGAG
 TCCGTGATCTGTCTCGGTTGCGGCTGACCGACGGGAGTGGCACCACTGCTGATCGAGCTGAAGAATGTTAAGGAGGA
 CAGTGAAGATGAGCACTTGGTACCATGACCTTGGATATGGATGGACAGAACAAAGGAGATATCGGGGCACTGCTTC
 CCGGCTGACGGTAAGGAGCGTGGTGGTGGAGGCGCTCTTGAAGACAAGGTCTCCGTGCGCCCTGGATTCCGAGTGC
 ATGACGGGAGTGAGGATGGGGGGACGCCACCAACGTGCCACCTGAAATGAACAACGCCTCAAGGTGAGGGTGA
 CCACGGCTGTGATGTGGACGACCCCTGTACCTCGAGCCCTGTCCCCCAATAGCCGCTGCCACGACGCTGGAGGACT
 ACAGCTGCGCTGTGACAAGGGTACCTTGGAAATAACTGTGTGGATGCTGTACCTGAACCCCTGCGAGAACATGGGG
 GCTGCTGCGCTCCCCCGCTCCCCGACGGCTACGTGTGCGAGTGTGGGCCAGTCACTACGGGCCGTACTGTGAGAA
 CAAACTCGACCTTCCGTGCCCCAGAGGCTGTGGGGGAACCCGCTGTGGACCTGCCACTGTGCCGTGACCAAGGCT
 TTGATCCCGACTGTAATAAGACCAACGGCCAGTGCCAATGCAAGGAGATTACTACAAGCTCCTAGCCACGACACCTGT
 CTGCCCTGCGACTGCTTCCCCATGGCTCCACAGCCGCACTTGGACATGGCCACCGGGCAGTGTGCTGCAAGCCGG
 CGTCATCGGCCCGCAGTGAACCGCTGCGACAACCCGTTGCCGAGGTACACGCTCGGCTGTGAAGTGTATACAATG
 GCTGTCCAAAGCATTTGAGGCCGGCATCTGGTGGCCACAGACCAAGTTCCGGCCAGCCGCTTCCGCTGCCATGCCCTAAG
 GGATCCGTTGGAATCGGCTCCGACACTGCAAGCGGGGAGAAGGGCTGGCTGCCCCAGAGCTCTTTAACTGTACACCAT
 CTCCTTCTGGACCTCAGGGCCATGAATGAGAAGCTGAGCCGAATGAGACGAGGTGGACGGCGCCAGGGCCCTGACG
 TGGTGAAGGGCCCTGCCACTGCTACACAGCACACGGGACGCTCTTTGGCAATGACGTGCGCACGGCTTACAGCTGCTG
 GGCCACGTCTTTCAGCACGAGAGCTGGCAGCAGGGCTTCGACCTGGCAGCCACGACGAGGACGCCGACTTTCACGAGGACGT
 CATCCACTCGGGCAGCGCCCTTCTGGCCCCAGCCACAGGGCGGCTGGGAGCAGATTCAGCGGAGCGAGGGCGGCACGG
 CACAGCTGCTCCGGCGCTCGAGGGCTACTTCAAGAACGTGGCACCAACGTGCGCGGACGTTACCTGCGGCCCTTCTGTC
 ATCGTACCGCCAACATGATTTCTGTGTCGACATCTTGAAGTTCAACTTTACGGGAGCCAGGGTCCCGGATTCGA
 CACCATCCATGAAGGATTTCCCGAGGCTGGAGTCTCCGCTCTCTTCCAGCCGACTTCTTACAGACCTGAAGAAA
 AAGAAGGCCCTGCTGAGGCGGGCTGGCCGGAGGACCAACCGGACGACCGCGCCGGGGCTGGACCGGAGGAG
 GCGCCGATCAGCAGGCGGAGGCGACACCTGATGACGCTGGCCAGTTCCGCGTCTGCTGTGCTCATCATTTACCGCACCT
 GGGGACGCTCTGCGCGAGCGCTACGACCCGACCGTCCGAGCTCCGGTTGCTTACCGGCCCATCATTAATACCCCGA
 TGGTGAACAGCTGGTGTACAGGAGGGGGCTCCGCTCCCGAGACCCCTGGAGAGGCCCGTCTGGTGGAGTTCCGCTG
 CTGGAGGTGGAGGACGCAACCAAGCTTGTCTGCGTGTCTGGAACCACTCCCTGCCCGTCTGTGGACGGGAGGGTGGTC

FIG. 1 Continued

TGCCCCGGGGCTGCGAGCTCCTGTCCAGGAACCGGACACATGTCCCTGCCAGTGCAGCCACACAGCCAGCTTTGCCGTGC
TCATGGATATCTCCAGCCGTGAGAACCGGGAGGTCTGCCCTCTGAAGATTGTACCTATGCCCGCTGTCTCCTTGTCACTG
GCAGCCCTGCTGCTGGCCTTCCTCTCCTGAGCCTGCTCCGCATGCTGCGCTCCAACCTGCACAGCAATTCACAAGCACCT
CGCCGTGCGCTCTTCTCTCTCAGCTGGTGTTCGTGATTGGGATCAACCAGACGGAAACCCGTTTCTGTGCACAGTGG
TTGCCATCCTCCTCCACTACATCTACATGAGCACCTTTGCCCTGGACCTCCTGGAGACCTGCATGTCTACCGCATGCTG
ACCGAGGTGCCAACATCGACACGGGGCCCATGCGGTCTACTACGTCGTGGGCTGGCGCATCCCGGCCATTGTACAGG
ACTGGCGGTGCGCCTGGACCCCCAAGGCTACGGGAACCCCGACTTCTGCTGGCTGTGCTTCAAGACACCTTGATTGGA
GCTTTGCCGGGGCCCATCGGAGCTGTTATAATCATCAACACAGTCACCTTCTGTCTATCTGCAAAGGTTTCTGCCAAAGA
AAGCACCATTAATTATGGGAAAAAAGGGATCGTCTCCCTGCTGAGGACCOCATTCTCTGCTGCTGCTCATCAGCGCCAC
CTGGCTGCTGGGGCTGCTGGCTGTGAACCGCGATGCACTGAGCTTTCACCTACCTCTTCCCATCTTCAGCGCTTACAGG
GCCCCCTCGTCTCTCTTTTCCACTGCGTCTCAACCAGGAGGTCCGGAAACACCTGAAGGGCGTCTCGGCGGGAGGAAG
CTGCACCTGGAGGACTCCGCCACACAGGGCCACCCTGCTGACGCGCTCCCTCAACTGCAACACCACCTTCGGTGACGG
GCTTGACATGCTGCGACAGACTTGGGCGAGTCCACCGCTCCTGAGACAGCATCTGTCAGGGATGAAGGGATCCAGAAGC
TCGGCGTGTCTCTGGGCTGGTGAGGGGACAGCCACGGAGAGCCAGACGCGTCCCTCATGCCCAGGAGCTGCAAGGATCCC
CCTGCCACGATTCGCACTCAGATAGCGAGCTGTCCCTGGATGAGCAGAGCAGCTCTTACGCTCTCTCACACTCGTCAGA
CAGCGAGGACGATGGGGTGGGAGCTGAGGAAAAATGGGACCCGGCCAGGGGCGCCGTCCACAGCACCCCAAAGGGGACG
CTGTGGCCAAACACGTTCCGGCCGGCTGGCCCGACAGAGCTGGCTGAGAGTGACAGTGAGGACCCACAGCGGCAAGCCC
CGCTGAAGGTGGAGACCAAGGTACGCTGGAGCTGCACCGCGAGGAGCAGGGCAGTCACCGTGGAGAGTACCCCCCGGA
CCAGGAGAGCGGGGGCGAGCCAGGCTTGCTAGCAGCCAGCCCCAGAGCAGAGGAAAGGCATCTTGAAAAATAAAGTCA
CCTACCCGCGCGCTGACGCTGACGGAGCAGAGCTGAAGGGCCGGCTCCGGGAGAAGCTGGCCGACTGTGAGCAGAGC
CCCACATCCTCGGACAGCTCTTCCCTGGGCTCTGGCGGGCCCCGACTGCGCCATCACAGTCAAGAGCCCTGGGAGGGAGCC
GGGCGTGACCACTCAACGGGTGGCCATGAATGTGCGACTGGGAGCCCCAGGCCGATGGCTCCGACTCTGAGAAAC
CGTGA

FIG. 2

MAPPPPVFLVLLLLAAAAALPAMGLRAAAWEPRVPGGTRAFALRPGCTYAVGAACTPRAPRELLDVGDRGLAGRRRV8
 CACRPLPLQVRLVARSAPTALSRRRLRARTHLPGCGARARLCGTGARLCGALCFVPGGCAAAQHSALAAPITLPAACRCPP
 RPRPRCPGRPICLPPGGSVRLRLCALRAAGAVRVGLALEAATAGTPSASPSPPPLPPNLPEARAGPARRARRGTSGR
 GSLKPPMPNYQVALPENEPAGTLILQLHAHYTIEGESEERSYMEGLFDERBRGYFRIDSATQAVSTDSVLDRETKETHV
 LRVKAVDYSTPPRSATTYITVLVKDTNDHSPVFEQSEYRERVRENLEVGVEVLTIRASDRDSPINANLRYRVLGGAWDV
 QLNESGCVVSTRAVLDRERAAEYQLLVEANDQGRNPGPLSATATVYIEVEDENDNYPPQSEQNYVVQVPEVDGLNTAVLR
 VQATDRDQGGONAAIHYSILSGNVAGQFYLHSLSGILDVINPLDFEDVQKYSLSIKAQDGRPPPLINSSGVVSVQVLDVND
 NEPIFVSSPPQATVLENVPLGYFVVHIQAVDADSGENARLHYRLVDTASTFLGGGSAGPKNPAPTDFPFQIHNSGWT
 VCAELDREVEHYSPFGEAVDHGSPPMSSSTSVSITVLVDNDNDPVFTQPTYELRLNEDAAVQSSVLTQLQARDRANSVI
 TYQLTGGNTRNRFALSSQRGGGLITLALPLDYKQEQYVLAVTA\$DGT\$RSHTAHVLINVT\$DANTHR\$VFPQ\$SHYTVSVSE
 DRPVGTSIATLSANDEDTGENARITYYIQDFVPQFRIDPDSGTMYTMMELDYENQVATILTMAQDNGIPKSDT\$TTLEI
 LILDANDNAPQFLWDFYQGSIPEDAPPETSILQV\$ATDRD\$GPNORLLYTFQGGDGDGDGYIEPTSGVIRTQRRLDREN
 VAVYNLWALAVDRGSPTPLSASVEIQVTILDINDNAPHEKDELEL\$VEENN\$FVGSV\$VAKIRANDPDEGPNAQIMYQIVE
 GDMRHFPQLDLLNGDLRAMVELDFEVRREYVLVVQATSAPLVSRATVHILLVDQNDNPFVLPDFQILFNNYVTNKSNSFP
 TQVIGCI\$AHDPDVSDSLMYTFVQGNELRLLLLDPATGELQLSRDLDMNRPL\$EALMEVSVSDGIH\$VTA\$PCTL\$RVTIITD
 DMLTNSITVRLNMSQEKFL\$PLALFVEGVAAVLSTTKDDV\$FVFNQNDT\$VSSN\$ILNVTF\$SALLPGGV\$RQGF\$P\$SED
 QEQIYLNRLT\$TTISTQRVLEP\$DDNICL\$REPCENYMKCV\$VLRFD\$SAPFL\$STTVLFRP\$IH\$INGLRCRC\$PPGFTGDYC
 ETEIDLCYSDPCGANGRCR\$REGGYTCECFEDFTGEHCEVDARS\$GRCANGVCKNGGTCVNLLIGGFHCVC\$P\$GEYERFPC
 EVTTR\$P\$PQ\$P\$VTFRGLRQR\$FHTISLTFATQERNGLLLYNGR\$FNEKHDFIALEIVDEQVQLTFSAGET\$TTT\$VAPKVP\$
 GVSDGRWHSVQVQY\$Y\$NKPNI\$GHLGLPHG\$P\$G\$EKMAV\$V\$VDDCDT\$TMAV\$RFGKDIGNY\$SCAAQGTQ\$T\$GSKSLDLT\$G\$PLLL
 GGVNPLPEDF\$PVHNRQ\$FVGCMRNL\$VDGK\$NVDMAGFIANNGTREGCAARRNFC\$DGRRCQNGGTCVN\$RWNYLCECPLRFG
 GKNC\$EQAMP\$P\$QLFSGESV\$V\$WSDLNIIISVFWYLG\$LMFTRKEDSVLMEAT\$SGGPT\$P\$RLQILNNYLOF\$V\$SHGPS\$DVB
 SVML\$GLR\$VTDGEWHLLI\$ELKNVKED\$EM\$CHLVTMTLDYCMDQNKADIGGMPLGLTVRSV\$V\$VGGASEDKV\$V\$RGRGRC
 MQGV\$RNGCTPT\$NVATLNMN\$NALKVRVKDGC\$D\$VDDPCTSS\$PCPPNSRCHDAWEDY\$SCVCDKGYLGIN\$C\$VDACHLNPCENMO
 ACVR\$P\$GSPQGYVCECGP\$SHYGPYCENKLDLPCPRG\$W\$GNEFVCGPCHCAV\$SKGFD\$PDCNK\$TNGQCQCKENY\$Y\$KLLAQDTC
 LPCDC\$P\$PHG\$SHRTCDMATGQCACKPGVIGRQCNRCDNPPAEVTTLGCEVITYNGC\$PKAFEAGI\$W\$PQT\$KFCQ\$PAAVPCPK
 GSVGN\$AVRHC\$SGEKGWLPPEL\$FNCTTISFVDLRAMNEKLSRNETQVDCARALQLV\$RALSATQHTGT\$FGNDV\$RTAYQLL
 GHVLOHESWQ\$Q\$GFLAATQDADFHEDV\$HSCSALLAPATRAAWEQIQRSEGGTAQLLRLECYF\$SNVARNV\$RTYLRPFV
 IVTANMILAVDIFDKFNFTGARVPRFDTIHREFFPRELESSV\$FPADFFRPPEEKEG\$P\$LLRPAGRRTTPQTRPGP\$GTERE
 APISRRRRHPDDAGQFAVALV\$IIYRTLQQLLPERYD\$PDRSLRLPHRPIINTPMVSTLVYSEGAPLPRPLERPVLEFAL
 LEVEERTK\$PVCVFWNH\$BLAVGGTGGWSARGCELLSRNRTHVACQC\$HTASFAVLMDISRRENGEVLPLKIVTYAAV\$SLSL
 AALLVAPVLLSLVRMLRSNLHSIHKHLAVALFLSQLV\$FVIGINQ\$TENPFLCTVVAILLHYIYNSTPAWTLVESLHVYRL

TEVRNIDTQPMRFY\$Y\$VVGWGI\$PAIVTGLAVGLDPQGYGNP\$DFCWL\$SLQDTL\$W\$SFAGPI\$GAVIIINTVTSVLSAKV\$SCQR
 KHHY\$Y\$GKKGIV\$SLLR\$TAF\$LLLLISATWLLQLLAVNRDALS\$FHYLFAIF\$SGLQGP\$FVLLFHCVLNQ\$EVRKHLK\$GVLGGRK
 LHL\$EDSAT\$TRATLLTR\$SLN\$CMTT\$FGDGP\$DMLRTDLGESTASLDSIVRDEGIQKLGVSSGLVRG\$SHGEPDASLMPR\$SC\$KDP
 PCHSDSDSEL\$SLDEQSS\$Y\$ASSHSS\$D\$EDDGVGAEEKWD\$PARCAVH\$STPKGD\$AVANHV\$PAGWPDQ\$SLAESD\$SED\$PSQKP
 RLK\$VETKV\$VELHREBQ\$G\$SHRGEY\$P\$PDQESGGAARLASSQ\$PPEQRKGILKNKVTY\$P\$P\$P\$TLTEQTLK\$RLREKLADCEQS
 PTSSRTSSLSG\$GGP\$DCAITV\$K\$PGREFGRDHLANGVAMNVRTG\$SAQADG\$SDSEK\$P

FIG. 3

Score = 939 (140.9 bits), Expect = 4.0e-81, Sum P(3) = 4.0e-81
Identities = 203/218 (93%), Positives = 203/218 (93%), Strand = Plus / Plus

Query: 230 CTGTAATAAGACCAACGCCAGTGCCAAT-GCAAGGAGAATTACTACAAGCTCCTAGCCC 288
CTG A T A A C GCC TG C T GCA GGAGAATTACTACAAGCTCCTAGCCC
Sbjct: 38281 CTGAAGTCACAGGCCCTGCCCTCTGGCTTTTGCA-GGAGAATTACTACAAGCTCCTAGCCC 38339

Query: 289 AGGACACCTGTCTGCCCTGCCGACTGCTTCCCCCATGGCTCCCACAGCCGCACTTGCGACA 348
AGGACACCTGTCTGCCCTGCCGACTGCTTCCCCCATGGCTCCCACAGCCGCACTTGCGACA
Sbjct: 38340 AGGACACCTGTCTGCCCTGCCGACTGCTTCCCCCATGGCTCCCACAGCCGCACTTGCGACA 38399

Query: 349 TGGCCACCGGGCAGTGTGCCTGCAAGCCCGGCGTCATCGGCCGCCAGTGCAACCGCTGCG 408
TGGCCACCGGGCAGTGTGCCTGCAAGCCCGGCGTCATCGGCCGCCAGTGCAACCGCTGCG
Sbjct: 38400 TGGCCACCGGGCAGTGTGCCTGCAAGCCCGGCGTCATCGGCCGCCAGTGCAACCGCTGCG 38459

Query: 409 ACAACCCGTTTGCCGAGGTCACCACGCTCGGCTGTGAAG 447
ACAACCCGTTTGCCGAGGTCACCACGCTCGGCTGTGAAG
Sbjct: 38460 ACAACCCGTTTGCCGAGGTCACCACGCTCGGCTGTGAAG 38498

FIG. 4

Score = 1000 (352.0 bits), Expect = 2.4e-98, P = 2.4e-98
Identities = 162/186 (87%), Positives = 172/186 (92%), Frame = +3

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Query:      3 YLGINCVDACHLNPCENMGACVRSPGSPQGYVCECGPSHYGPYCENKLDLPCPRGWGWP 182
              Y G  CVDAC LNPC+++ ACVRSP +P+GY CECCP HYG YCENK+DLPCP+GWWGWP
Sbjct: 1917 YFGKKCVDACLLNPCKHVAACVRSPNFPFGYSCECGPGHYGQYCENKVDLPCPKGWWGWP 1976

Query:     183 VCGPCHCAVSKGFDPCNKTNQGQCCKENYYKLLAQDTCLPCDCFPHGSHSRTCDNATGQ 362
              VCGPCHCAVS+GFDPCNKTNQGQCCKENYYK AQD CLPCDCFPHGSHSR CDM TCQ
Sbjct: 1977 VCGPCHCAVSQGFDPDCNKTNQGQCCKENYYKPPAQDACLPDCFPHGSHSRACDMDTGQ 2036

Query:      61 CCTGCGTGCGCTCCCCCGGCTCCCCGCAGGGCTACGTGTGCGAGTGTGGGCCCCAGTCACT 120
              |||
Sbjct: 33445 CCTGCGTGCGCTCCCCCGGCTCCCCGCAGGGCTACGTGTGCGAGTGTGGGCCCCAGTCACT 33504

Query:     121 ACGGGCCGTACTGTGAGAACAA 142
              |||
Sbjct: 33505 ACGGGCCGTACTGTGAGAACAA 33526
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FIG. 5

Score = 12924 (4549.5 bits), Expect = 0.0, P = 0.0
Identities = 2451/3034 (80%). Positives = 2677/3034 (88%)

Query: 1 MAPPPFPVLPVLLLLAAAAALPAMGLRAAAWEPRVPGGTRAFALRPGCTYAVGAAC TFR- 59
MAP P VLP L+LLAAAA LPA+ L AAWE RVFGG RAFAL PG +Y + TFR
Sbjct: 1 MAPSSPRVLPALVLLAAAA-LPALELGAAAWELRVFGGARAFALGPGWSYRLDTTRTFRE 59

Query: 60 ---APRELLDVGRD-GRLAGRRRVSG-AGRPLPLQVRLVARSAPTALSRRRLRARTHLPGC 114
RE GR G AG + AGR LPLQVRLVAR APTA S LRAR + C
Sbjct: 60 LLDVSREGPAAGRRLGLGAGTLGCARLAGRLPLQVRLVARGAPTAPSLVLRARAYGARC 119

Query: 115 GARA-RLCGTGARL-----CG-ALCFFVPGGCAAAQKSALAAPTTL PACRCPPRP 162
Q R R GA L G ALCFP GG AA+ S L A T PAC CPP
Sbjct: 120 QVRLRLRSARGAELRSPAVRSVPGLGDALCFPAAGGGAASLTSVLEAITNFPACSCPPVA 179

Query: 163 RPRCPGRPICLPFGGSVRLRLCALRRAGAVRVGLALEAATAGTPSASPSPPPLPNL 222
C PICL PGGS LRL+CAL RAAGAV V L ++A T+OTPS SPS SP L NL
Sbjct: 180 GTGCRRGPICLRPGGSALRLVLCALGRAAGAVVVELVQA-TSGTPSESFSVSPSLL-NL 237

Query: 223 PEARAGPARRARRGTSGRQSLKFPMPNYQVALFENEPAGTILILQLHAHYTIEGEEERVS 282
+ RAG RR+RRCT S +FP+P+YQV++ ENEPAGT +++L AH EG+ R+SY
Sbjct: 238 SQPRAGVVRRSRRGTGSSTSPQFPLPSYQVSVPENEPAGTAVIELRAHDPDEGDAGRLSY 297

Query: 283 YMEGLFDESRGYFRIDSATGAVSTDSVLDRETKETHVLKAVDVSTPFRSATTYITVL 342
ME LFDERS GYF ID+ATGAV+T LDRETK+THVL+V AVD+ +P RSA TY+TV
Sbjct: 298 QMEALFDESRNGYFLIDAATGAVTTARSILDRETKDTHVLKVS AVDHGSPRRSAATYLTVT 357

Query: 343 VKDTNDHSPVFEQSEYREVRVRENLEVGVEVLTIRASDRSPINANLRYRVLGGAWDVFL 402
V DTNDHSPVFEQSEYRER+RENLEVGVEVLTIRA+D D+P NAN+RYR+L GA VF++
Sbjct: 358 VSDTNDHSPVFEQSEYRERIRENLEVGVEVLTIRATDGDAPSNNMRYLLEGAGGVFEI 417

Query: 403 NESSCVVSTRAVLDRREAAEYQLLVEANDQGRNPGPLSATATVYIEVEDENDNYPQFSEQ 462
+ SGVV TRAV+DREAAEYQLLVEANDQGRNPGPLSA+ATV+I VEDENDNYPQFSE+
Sbjct: 418 DARGSVVTRAVVDREAAEYQLLVEANDQGRNPGPLSASATVHIVVEDENDNYPQFSEK 477

Query: 463 NYVVQVPEDVGLNTAVLRVQATDRDQGNAAIHYSILSGNVAGQFYLHSLSGILDVINPL 522
YVVQVPEDV +NTAVLRVQATDRDQGNAAIHYSI+SGN+ GQFYLHSLSG LDVINPL
Sbjct: 478 RYVVQVPEDVAVNTAVLRVQATDRDQGNAAIHYSIVSGNLKGQFYLHSLSGSLDVINPL 537

Query: 523 DFEVQKYSLSIKAQDGGRPPLINSSGVSVQVLDVNDNEPIFVSSPPQATVLENVPLGY 582
DFE +++Y+L IKAQDGGRPPLINSSG+VSVQVLDVNDN PIFVSSPPQA VLENVPLG+
Sbjct: 538 DFEAIREYTLRIKAQDGGRPPLINSSQLVSVQVLDVNDNAPIFVSSPPQA AVLNVPLGH 597

Query: 583 PVVHIQAVDADSGENARLHYRLVDTASTTLGGGSAGPKNPAPTDFPFQIHNSSGMITVC 642
V+HIQAVDAD+GENARL YRLVDTAST +GG 6 +NPA PDFPFQIHNSSGMITVC
Sbjct: 598 SVLHIQAVDADAGENARLQYRLVDTASTIVGSSVDSNPASAPDFPFQIHNSSGMITVC 657

Query: 643 AELDREEVEHYSFGVEAVDHGSPMSSSTSVSITVLDVNDNDPVFTQPTYELRLNEDAAV 702
AELDREEVEHYSFGVEAVDHGSP M888 SVSITVLDVNDNDP+FTQP YELRLNEDAAV
Sbjct: 658 AELDREEVEHYSFGVEAVDHGSPAMSSSASVSITVLDVNDNDPMFTQPFVYELRLNEDAAV 717

Query: 703 GSSVLTLOARDRDANSVITYQLTGGNTRNRFALSSQGGGLITLALPLDYKQEQQYVLAV 762
GSSVLT/L+ARDRDANSVITYQLTGGNTRNRFALSSQ GGGGLITLALPLDYKQEQ+QYVLAV
Sbjct: 718 GSSVLT/LRARDRDANSVITYQLTGGNTRNRFALSSQSGGLITLALPLDYKQERQYVLAV 777

Query: 763 TASDGTASHTAHVLINVT DANTHRPFVQSSHYTVSVSEDRFVGTSIATLSANEDTGENA 822
TASDGTASHTA V INVT DANTHRPFVQSSHYTVSVSEDRFVGTSIAT+SA DEDTGENA
Sbjct: 778 TASDGTASHTAQVF INVT DANTHRPFVQSSHYTVSVSEDRFVGTSIATISATD EDTGENA 837

Query: 823 RITYVTQDPVPQFRIDPDSGTMYTMMELDYENQVAYTLTMAQDNGIPQKSDTTTLEILI 882
RITYV++DPVPQFRIDPD+GT+YTM ELDYEQ AYTL I AQDNGIPQKSDTT+LEILI
Sbjct: 838 RITYVLEDVPVPQFRIDPDGTGTIYTMELDYEDQAAYTLAITAQDNGIPQKSDTTSLLEILI 897

FIG. 5 Continued

Query: 883 LDANDNAPQFLWDFYQGSIFEDAPPSTSIQVSATDRDSGPNGRLLYTFQGGDDGDGDFY 942
 LDANDNAP+FL DFYQGS+FEDAPPSTS+LQVSATDRDSGPNGRLLYTFQGGDDGDGDFY
 Sbjct: 898 LDANDNAPRFLRDFYQGSVPEDAPPSTSVLQVSATDRDSGPNGRLLYTFQGGDDGDGDFY 957

Query: 943 IEPTSGVIRTQRRLDRENVAVYNLWALAVDRGSPPLSASVEIQVTILDINDNAPMFEKD 1002
 IEPTSGVIRTQRRLDRENVAVYNLWALAVDRGSP PLSASV IQV++LDINDN P+FEKD
 Sbjct: 958 IEPTSGVIRTQRRLDRENVAVYNLWALAVDRGSPNPL\$ASVGIQVSULDINDNPFVFEKD 1017

Query: 1003 EELFVEENPVGSSVAKIRANDPDEGPNQIMYQIVEGDMRHHFQLDLLNGDLRAMVEL 1062
 EELFVEEN+PVGSSVA+IRANDPDEGPNQI+YQIVEG++ FQLDLL+GDIRA+VEL
 Sbjct: 1018 EELFVEENSPVGSSVARIRANDPDEGPNQIYQIVEGNVPEVFQLDLLSGDLRALVEL 1077

Query: 1063 DFEVRREYVLVQATSAPLVSRAVHILLVDQNDNPFVLPDFQILFNNTVTKSNSFPPTG 1122
 DFEVRR+Y+LVVQATSAPLVSRAVHI L+QNDNPF LPDFQILFNNTVTKSNSFP+G
 Sbjct: 1078 DFEVRDYMVLVQATSAPLVSRAVHIRLLDQNDNPFELPDFQILFNNTVTKSNSFP+G 1137

Query: 1123 VIGCIPAHDPDVSLSNYTFVQGNELRLLLDPATGELQLSRDLNDRPLEALMEVSVSD 1182
 VIG IPAHDPD+SDLSNYTF+QGNEL LLLDPATGELQLSRDLNDRPLEALMEVSVSD
 Sbjct: 1138 VIGRIPAHDPDLSLSNYTFVQGNELSLLLDPATGELQLSRDLNDRPLEALMEVSVSD 1197

Query: 1183 GIHSVTAFCTLKVTIITDDMLTNSITVRLNMSQEKFLSPLLALFVEGVA AVLSTTKDDV 1242
 GIHSVTA CTLKVTIITDDMLTNSITVRLNMSQEKFLSPLL+LFVEGVA VLSTTKDD+
 Sbjct: 1198 GIHSVTALCTLKVTIITDDMLTNSITVRLNMSQEKFLSPLLALFVEGVATVLSTTKDDI 1257

Query: 1243 FVFNQNDTDVSSNINLVTFSSALLPGGVRGQFPSEDLQEIQYILNRTLLTTISTQRLPFP 1302
 FVFN+QNDTDVSSNINLVTFSSALLPGG RQ+FPSEDLQEIQYILNRTLLTTIS QRLPFP
 Sbjct: 1258 FVFNQNDTDVSSNINLVTFSSALLPGGTRGRFPSEDLQEIQYILNRTLLTTISQRLPFP 1317

Query: 1303 DDNICLREPCENYMKCVSVLRFDSAPFLSSTTVLFRPIHPINGLRRCRCPGFTGDCYET 1362
 DDNICLREPCENYMKCVSVLRFDSAPF+SSTTVLFRPIHPI GLRCRCRCPGFTGDCYET
 Sbjct: 1318 DDNICLREPCENYMKCVSVLRFDSAPFISSTTVLFRPIHPITGLRCRCPGFTGDCYET 1377

Query: 1363 EIDLCSYSDPCGANGRCRSREGGYTCECFEDFTGEHCVDARSGRCA+GVCKNGGTCVNLL 1422
 EIDLCSY+PCGANGRCRSREGGYTCECFEDFTGEHC+V+ RSGRCA+GVCKNGGTCVNLL
 Sbjct: 1378 EIDLCSYSDPCGANGRCRSREGGYTCECFEDFTGEHCQVNVRSGRCA+GVCKNGGTCVNLL 1437

Query: 1423 IGGFHCVCPPGEYERPYCEVTTRSFPPQSFVTFRGLRQRFHFTISLTFATQERNGLLLYN 1482
 IGGFHCVCPPGEYE PYCEV+TRSFPPQSFVTFRGLRQRFHFT+SL FATQ+RN LLLYN
 Sbjct: 1438 IGGFHCVCPPGEYEHFYCEVSTRSFPPQSFVTFRGLRQRFHFTVSLAFATQDRNALLYN 1497

Query: 1483 GRFNEKHDFIALBIVDEQVQLTFSAGETTTTVA PKVPSGVSDGRWHSVQVQYNNKPNIGH 1542
 GRFNEKHDFIALBIV+EQ+QLTFSAGETTTTV P+VP GVSDGRWHSV VQYNNKPNIGH
 Sbjct: 1498 GRFNEKHDFIALBIVEBQLQLTFSAGETTTTVPQVPGGVSDGRWHSVQVQYNNKPNIGH 1557

Query: 1543 LGLPHGPSGEKMAVVTVDCCDTMAVRFGKDIGNYSCAAQGTQTSKKSLLDTGPLLLGG 1602
 LGLPHGPSGEK+AVVTVDCCD +AV FG +GNYSCAAQGTQ+GSKKSLLDTGPLLLGG
 Sbjct: 1558 LGLPHGPSGEKVAVVTVDCCDAVAVHFGSYVGNYSCAAQGTQSGSKKSLLDTGPLLLGG 1617

Query: 1603 VPNLPEDFPVHNRQFVGCNRNLSVDGKNVDMAGFIANNGTREGCAARRNFCDGRRCCQNGG 1662
 VPNLPEDFPVH+RQFVGCNRNLS+DG+ VDMA FIANNGTREGCAARRNFCDGRRCCQNGG
 Sbjct: 1618 VPNLPEDFPVHSRQFVGCNRNLSIDGRIVDMAFIANNGTREGCASQRNFCDGRRCCQNGG 1677

Query: 1663 TCVRNRMNYLCECLRFGGKNCEQAMPHPQLFSGESVVSWSLDNIIISVPWYLGIMFRTR 1722
 TCVRNRM NYLCECLRFGGKNCEQAMPHPQ P+GESVW WSDL+I ISVPWYLGIMFRTR
 Sbjct: 1678 TCVRNRMNYLCECLRFGGKNCEQAMPHPQRFTGESVVLWSDLDITISVPWYLGIMFRTR 1737

FIG. 5 Continued

Query: 2563 VRNIDTGPMRFYVVGWGIPAIVTGLAVGLDPQGYGNPFCWLSLQDTLIWSFAGPIGAV 2622
VRNIDTGPMRFY+VVGWGIPAIVTGLAVGLDPQGYGNPFCWLSLQDTLIWSFAGP+G V

Sbjct: 2578 VRNIDTGPMRFYHVVGWGIPAIVTGLAVGLDPQGYGNPFCWLSLQDTLIWSFAGPVGTV 2637

Query: 2623 IIINTVTSVLSAKVSCQRKHYYGKKGIVSLLRTAFLLLLISATWLLGGLAVNRDALSF 2682
IIINTV VLSAKVSCQRKHYY +KG+VS+LRTAFLLLL++ATWLLGGLAVN D LSF

Sbjct: 2638 IIINTVIFVLSAKVSCQRKHYYERKGVVSMRLTAFLLLLVTATWLLGGLAVNSDTLSF 2697

Query: 2683 HYLFAIFSGLQGFVLLFHCVLNQEVKHLKGVLCGRKLHLED SATTRATLLTRSLNCNT 2742
HYLFA FS LQC FVLLFHCV ++EVRKHL+ VL G+KL L+DSATTRATLLTRSLNCN

Sbjct: 2698 HYLFAAFSCLQGIFVLLFHCVAHREVRKHLRAVLAGKKQLDSDSATTRATLLTRSLNCNN 2757

Query: 2743 TFGDGPDMRLRTDLGESTASLDSIVRDEGIQKLGVS SGLVRGSHGEPDASLMPSRCKDPFG 2802
T+ +GPDMLRT LGESTASLDS RDEG+QKL VSSG RG+HGEPD S +PR+ K G

Sbjct: 2758 TYSEGPDMLRTALGESTASLDSTTRDEGVQKLSVSSGPARGNHGEPDTSFIPRNSKKAHG 2817

Query: 2803 HDSDSDSELSLDEQSSSYASSHSSDSEDDGVGAEEKWDPARGAVHSTPKGDAVANHVPA 2862
DSDSDSELSLDE SSSYASSH+SDSEDDG AE+KW+PA G HSTPK DA+ANHVPA

Sbjct: 2818 PDSDSDSELSLDEHSSSYASSHTSDSEDDGGEAEDKWNPAAGPAHSTPKADALANHVPA 2877

Query: 2863 WPDQSLAESDSEDPSGKPRKLVETKVSVELHREEQCSHRGEYPPDQESGGAAR---LASS 2919
WPD+SLA SDSE+ +P LKVETKVSVELHR+ QG+H G+ P D ESG A+ + SS

Sbjct: 2878 WPDESLAGSDSEELDTPEHLKVETKVSVELHRQAQGNHCQDRPSPESGVLAQFVAVLSS 2937

Query: 2920 QPPEQRKGILKNKVITYPPPLTLTEQTLKGRRLREKLADCEQSPTSSRTSSLGSG----GPD 2975
QP EQRKQILKNKVITYPPPL EQ LK RLREKLADCEQSPTSSRTSSLGSG D

Sbjct: 2938 QPQEQRKQILKNKVITYPPPLP--EQPLKSLRLREKLADCEQSPTSSRTSSLGSGDGVHATD 2993

Query: 2976 CAITVKSPPGREPGRDHLNGVAMNVRTGSAQADGSDSEKP 3014
C IT+K+P REPGR+HLNGVAMNVRTGSAQA+GSDSEKP

Sbjct: 2996 CVITIKTPRREPGRHLNGVAMNVRTGSAQANGSDSEKP 3034

FIG. 6 Continued

[illegible]

FIG. 6 Continued

[illegible]

FIG. 7

TGGAGTTTGTGCGGGCGCTGTGGCTGGGCCTGGCGCTGGCGCTGGGGCCGGGGTCCCGGGGGG
 ACCCTCAGCCGTGCGGGGTCTTGGCGCGCTCGGGGGCTCCGTGCGCTGGCGCGCCCTCTGCC
 CGCGCTCTCGCCCGCGCCCGCGCCCGCGCCCTGGCCCGGGCCCGCTGGCGCGCGGCTGCC
 CACAACCTGAGCTTGGAGCTGGTGGTGGCGCGCCCCCGCCCGGACCCCGCTCGCTGACCCG
 GCCTGTCCAGGCGCTGGTGGCTCCGGGGCTGGCGCCCTGCTCGCTTTCCCGAGGCTCGGCCG
 GCTGCTGCAGCTGCACTTCCTGGCGGGCGCCACCGAGAACCCCGTGTCTAGCTGCTGGCGGG
 GCGCGCGCGCCCTCGGAGCCCGGAACCCATTCCACTGCAGCTGCACTGGGCCAGCCCCCTGG
 GACGCTGCTGGATGTGCTGGTGGCGTGTCTGCAGGCGCACGCTGGGAAGAGCTCGGCCTGGCC
 GTGCCGCACTCAGGACCCCGCGGCGCTGGTGGCCCTCTGGACAAGCCGGGGCTGGCCGGCCCCAC
 GCTGGTCTTGGAACTAAGCCGGCGGGACACGGGAGATGCAAGACTGCGGGCACCCCTGGCCCCG
 GCGCGGCCAGTGGGGGGTGAAGCACCGGTACCCGCGGCGGTCTCTCTCGCTGTGACATCGCCC
 TGCCCGTCCGGTGTGGAGGCGGTACCTCCCGGCCCCACTGGCTGTGGGGACACCACTGCCGCG
 AAGGCCCTGCCACCCCGGGGCTGCCACAGGCTGTGGCGCTGGGCGAGGTGGCACGACCCCG
 CTGGAGGCGCCATCCATGACATTGTGCAACTGGTGGCCCGGGCTGGGCACTGCGGCCAGGT
 CAGCGAAGCGAGCCCTCTCCCGCCCCGGTCAACTGCGGGACCTGCAGCCGGCGGGCGCGA
 TCCCCGGGGCGCTTCTTGGCACGGTTCCTGGCCAACACGTCTTCCAGGGCGGCAAGGGCCCCGTG
 JGGTGACAGGCGCTCCCCAGACGAAGACGGGCGGTGCCAGCGGGGCGAGCTGTGCTGGACCT
 GCACCAACGACTCGGCCACCTGGACGCACTGTTCGCGCGCTGGCCAACGGCTCAGCGCCCCGT
 CCTGCGCAAGTGTGCTACGGCTACTGCATTGACCTGTGGAGCGGCTGGCGGAGGACACGCCC
 TCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGGCTGGGGACGGCCGCTGGACC
 GCCTGGTCCGGGACCTGCTGGCCGGCGGGGCCACATGGCGGTCAACAGCTTCAGTATCAACTCC
 CCGCTCACAGGTGGTGGACTTCACCAAGCCCTTCTTCTCCACAGCCTGGGCATCATGGTGGGG
 ACGGACACGGCTCACCATCGGTGCTTATGTGGCCCTGCACTGGTCCAGCTGGTGGGGCT
 TTTGGGGCCCTGCACCTCAACGCGCTCTTCTCTACCGTGTACGAGTGGCGTAGCCCCACGGCCT
 CGCCAGTGGCGGCAACCGCAGCACCGTCTTCTCTACTCTCAGCCCTCAACCTGTGCTACGCCA
 TCTCTTACAGCGCACCGTGTCCAGCAAGACGCCCAAGTGGCCACGGGGCGGCTGCTCATGAACCT
 TGGGCCATCTTCTGCTGTGTGCTGTCCAGCTACACGGCCAACCTGGCTCCCGTCATGGTGGG
 ACAAGACCTTCGAGGAGCTGTGGGGATCCACGAACCCCAAGGGCTTCCGCTTCGGCAACGTGTGG
 AGAGCAGCGCGAGGCGTACATCAAGAAGAGCTTCCCGACATGCACGCACACATCGCGCGCAC
 JCGCGCCACCAAGCCCCGCGGCGTCCCATGCTCACGAGCGACCCCCCAAGCTCAACGCCCTTC
 CATGGACAAAGTGGCTCTGGACTACGAGGTCTCATGACGCGGACTGCAAACTGCTGACCGTGG
 AAAGCCCTTCGCCATTGAGGGCTATGGGATCGGACTGCCCGAGAACTCGCCCTCACTCCAACT
 TCCGAGTTTATCAGCCGCTACAAAGTCTCTCGGCTTATCGACCTGCTCCACGACAAAGTGTACAAG
 TGGTGCTTGGCGCAAGCGGGTCTTTGCGGTTACAGAGACCTGCAGATGAGCATCTAACCTTCG
 JGGCTCTTGGTGTGTGCTGTGCTGGGCTGGGCGAGGCTGTGCTCAGCTCGCTGGGCGAGCACGC
 TCTTCCGCTTGGCGCTGGCGCGCATCCCAAGGGGAGCAGGCTGCACTACTGGCTGCACACAGC
 GAAAATCCACCGCGCCCTCAACACGGAGCCAOCAGAGGGGTGGAAGGAGGAGACGGCAGAGGC
 JAGGCCAGCGGCCCGGAGGTGGAGCAGCAGCAGCAGCAGGACCAAGCGCTCCGGAGG
 TGGAAACGGGGCGGCGCGGCGGTGGACAAGGAGCGCGCGTGGCGTTCTTGTGTGGAGGCGCGG
 GTTGTGGCAACCGAAGCGGACGCGGAGGCGGAGGCTGGCCCGGAGAGGGCCCCGTCTGGCTGT
 TCTACGGCGCGCGCGCGCGCAAGGCCACGGGGCCCCCGAGCCGGGGAGCTGCAGGAGC
 GAGCGCCCATCGAAGTGGCGGTGAGCGGCTCGGCGAGGCTGGTGGCGCGCGGCGAGCTCC
 GCACAGCTCGGGGACAGCGCACGTACCGGCTCGGGCTTGCTTCAAGCCAGAGCGCCCCCG
 GAGGCCCCACCACTCTGGCCGACCGGGGAGCCAGGAATGA

FIG. 8

IEFVRALWLGLALALGPGSAGGHPQPCGVLARLGGSVRLGALLPRAPLARARARAALARAALAPRI
LSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAFPEARPELLQLHFLAAATETPVL
SILRREARAP
QAPNFFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTQDPGGLVALWTSRAGRPPQ
VLDLS
RDTGDAGLRARLAPMAAPVGGHAPVPAAVLLGCDIARARRVLEAVPPGPHWLLGTPLFPK
ALFTAGLP
QLLALQEVARPFLEAAIHDIQVLVARALGSAAQVQPKRALLPAPVNCODLQAGPESPGRFL
ARFLANT
FQGRTPGVVWTGSSPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGY
CIDLLER
AEDTPFDL FELYLVDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS
PFFSTSLGI
IVRARDTASPIGAFMWPLHWSTWLGVFAALHLTALFLTVEYWRSPYGLTPRGRNRSTVFS
YSSALNLC
AILFRRTVSSKTPKCPTGRLLMNLWAFCLLVLSSTANLAAMVVGDKTFEELSGIHDPKGFR
FOTVWE
SAEAYIKKSFPDMHAHMRRHSAPTTPROVAMLTSDPPKLNAPIMDKSLLDYEVSIDADCKLL
TVGKPF
JEGYGIGLPQNSPLTSNLSEFISRYKSSGFIDLLHDKWYKMVPCGKRVPVAVTETLQMS
TYHFAGLFVLLC
GLGSALLSSLQEHAFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPFGSKEETA
EAEPSGPEVEQQQ
QDQPTAPEGWKRARRAVDKERRVRFLLEPAVVVAPEADAEAEAAPREGPVWLCSYORPPA
ARFTGAP
PGELQELERRIEVARERLRQALVRRGQLLAQLGDSARHRPRLLQARAAPAEAPPHSGRPGSQE

FIG. 9

Score = 3832 (575.0 bits), Expect = 0.0, Sum P(5) = 0.0
Identities = 928/1076 (86%), Positives = 928/1076 (86%), Strand = Plus / Plus

Query: 788 CACTGCCGCCCAAGGCCCTGCCACCGCGGGGCTGCCACCAGGGCTGCTGGCGCTGGGCG 847
C CTGCC CC A G CCTG CCA C CG CT CCA GC C GGC C G G G
Sbjct: 22736 CCCTGCC-CCTAGGTTCCCTGGCCAACACGTC-CTTCCAGGGCCGCA-CGGGCCCCGTGTG 22792

Query: 848 AGGTGGCAG-ACCCCCGCTGG-AGGCC-G-C-CATC-CATGACATTGTGCAACTGGTGG 901
GGTG CA G A C CC C GG A C G C C C C T A TGTG A C T G
Sbjct: 22793 -GGTGACAGGCAGTCC-CAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCT-TCG 22849

Query: 902 CCGGGGCGCT-GGGCAGTGGCGGCCAGGTGCAGCCGAAGCGAGCCCTCCTCCCCGCCCG 960
CC GG C C GGG G C G CC GG CA C G G AGC C C GCC G
Sbjct: 22850 CCGGACCCACGGGGCGCCCCGGCCTGGGCCA-CGGTGGGCAGCTGGCGGACGGCCA-G 22907

Query: 961 GTCAACTGCGGGACCTGCAGCCGGCGGGCCCGAGTCCCCGGGGCG-CTTCTTGCCACG 1019
T ACT GG ACC G AG G C GC CG G CCCCC C C TG C G
Sbjct: 22908 CTGGACTT--GGAACCGGGAGGTGCTCTGCACG-GCCCCCGCCCCCAGAGGGTGCCAG 22964

Query: 1020 GTTCCTGGCC-AA-CA-CGTCTTCCAGGGCCGCACGGGC-CCCGTGTGGGTGACAGGCA 1075
GT CTGGCC AA C CGT T A GC G G C CCC T TG GT G C
Sbjct: 22965 GT--CTGGCCCAAGCTGCGTG-TGGTAACGCTGTTGGAACACCCATTGTGTGTT--GCCC 23019

Query: 1076 GCTCCCCAGACGAAGACGGGCAAGTGGCCAGCGGGGAGCTGTGCCTGGACCCCTGGCACCA 1135
G CCAGACGAAGACGGGCAAGTGGCCAGCGGGGAGCTGTGCCTGGACCCCTGGCACCA
Sbjct: 23020 GTGATCCAGACGAAGACGGGCAAGTGGCCAGCGGGGAGCTGTGCCTGGACCCCTGGCACCA 23079

Query: 1136 ACGACTCGGCCACCTGGACGCACTGTTCGCCCGCGCTGGCCAACGGCTCAGCGCCCCGTG 1195
ACGACTCGGCCACCTGGACGCACTGTTCGCCCGCGCTGGCCAACGGCTCAGCGCCCCGTG
Sbjct: 23080 ACGACTCGGCCACCTGGACGCACTGTTCGCCCGCGCTGGCCAACGGCTCAGCGCCCCGTG 23139

Query: 1196 CCCTGCGCAAGTGTCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 1255
CCCTGCGCAAGTGTCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA
Sbjct: 23140 CCCTGCGCAAGTGTCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 23199

Query: 1256 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG 1315
CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG
Sbjct: 23200 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG 23259

Query: 1316 GCGCCTGGACCGGCTGGTCCGGGACCTGCTGGCCGGCCGGGCCCACATGGCGGTACCA 1375
GCGCCTGGACCGGCTGGTCCGGGACCTGCTGGCCGGCCGGGCCCACATGGCGGTACCA
Sbjct: 23260 GCGCCTGGACCGGCTGGTCCGGGACCTGCTGGCCGGCCGGGCCCACATGGCGGTACCA 23319

Query: 1376 GCTTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACAGCCCCCTTCTTCTCCA 1435
GCTTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACAGCCCCCTTCTTCTCCA
Sbjct: 23320 GCTTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACAGCCCCCTTCTTCTCCA 23379

Query: 1436 CCAGCCTGGGCATCATGGTGGGGGACGGGACACGGCCTCACCCATCGGTGCCTTTATGT 1495
CCAGCCTGGGCATCATGGTGGGGGACGGGACACGGCCTCACCCATCGGTGCCTTTATGT
Sbjct: 23380 CCAGCCTGGGCATCATGGTGGGGGACGGGACACGGCCTCACCCATCGGTGCCTTTATGT 23439

Query: 1496 GGCCCCTGCACTGGTCCACGTGGCTGGGCGTCTTTGCGGGCCCTGCACCTCACCGCGCTCT 1555
GGCCCCTGCACTGGTCCACGTGGCTGGGCGTCTTTGCGGGCCCTGCACCTCACCGCGCTCT

FIG. 9 Continued

Sbjct: 23440 GGCCCCCTGCACTGGTCCACGTGGCTGGGCGTCTTTGCGGCCCTGCACCTCACCGCGCTCT 23499

Query: 1556 TCCTCACCGTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA 1615
TCCTCACCGTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA

Sbjct: 23500 TCCTCACCGTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA 23559

Query: 1616 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA 1675
GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA

Sbjct: 23560 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA 23619

Query: 1676 CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCCGCCCTGCTCATGAACCTCTGGGCCA 1735
CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCCGCCCTGCTCATGAACCTCTGGGCCA

Sbjct: 23620 CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCCGCCCTGCTCATGAACCTCTGGGCCA 23679

Query: 1736 TCTTCTGCCTGCTGGTGCTGTCCAGCTACACGGCCAACCTGGCTGCCGTTCATGGTCGGGG 1795
TCTTCTGCCTGCTGGTGCTGTCCAGCTACACGGCCAACCTGGCTGCCGTTCATGGTCGGGG

Sbjct: 23680 TCTTCTGCCTGCTGGTGCTGTCCAGCTACACGGCCAACCTGGCTGCCGTTCATGGTCGGGG 23739

Query: 1796 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCAAGGGCTTCCGCTTCGGCACCG 1855
ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCAAGG C GC TCGG

Sbjct: 23740 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCAAGGTGGGCGGCCTCGGGGGG 23799

Query: 1856 TGTGGGAG 1863
TG GGG G

Sbjct: 23800 TGGGGGTG 23807

FIG. 10

Score = 2426 (854.0 bits), Expect = 0.0, Sum P(2) = 0.0
Identities = 463/474 (97%), Positives = 464/474 (97%), Frame = +1

```

Query: 1063 WVTGSSPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 1242
      +V    PDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER
Sbjct: 427 FVFARDPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 486

Query: 1243 LAEDTPPDFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 1422
      LAEDTPPDFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS
Sbjct: 487 LAEDTPPDFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 546

Query: 1423 PFFSTSLGIMVRARDTASPIGAFMNPLHNSWTLGVFAALHLTALFLTVEYWRSPYGLTPR 1602
      PFFSTSLGIMVRARDTASPIGAFMNPLHNSWTLGVFAALHLTALFLTVEYWRSPYGLTPR
Sbjct: 547 PFFSTSLGIMVRARDTASPIGAFMNPLHNSWTLGVFAALHLTALFLTVEYWRSPYGLTPR 606

Query: 1603 GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCTGRLLMNLWAI FCLLVLSSTANLAA 1782
      GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCTGRLLMNLWAI FCLLVLSSTANLAA
Sbjct: 607 GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCTGRLLMNLWAI FCLLVLSSTANLAA 666

Query: 1783 VMVGDKTFEELSGIHDPK-----CFRFGTVWESSAEAYIKKSFPDMHAMRRHSAPTTP 1944
      VMVGDKTFEELSGIHDPK          CFRFGTVWESSAEAYIKKSFPDMHAMRRHSAPTTP
Sbjct: 667 VMVGDKTFEELSGIHDPKLHHPAQGFRFGTVWESSAEAYIKKSFPDMHAMRRHSAPTTP 726

Query: 1945 RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPFATIEGYGIGLPQNSPLTSN 2124
      RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPFATIEGYGIGLPQNSPLTSN
Sbjct: 727 RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPFATIEGYGIGLPQNSPLTSN 786

Query: 2125 LSEFISRYKSSGFIDLLHDKWYKMPVCGKRVPFAVTETLQMSIYHFAGLFVLLCLGLGSAL 2304
      LSEFISRYKSSGFIDLLHDKWYKMPVCGKRVPFAVTETLQMSIYHFAGLFVLLCLGLGSAL
Sbjct: 787 LSEFISRYKSSGFIDLLHDKWYKMPVCGKRVPFAVTETLQMSIYHFAGLFVLLCLGLGSAL 846

Query: 2305 LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP 2466
      LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP
Sbjct: 847 LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP 900

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FIG. 11

[illegible]

FIG. 12

ATGGAAGTTTGTGCGGGCGCTGTGGCTGGGCGCTGGCGCTGGCGCTGGCGCGGGGTCCGCGGGGGGC
 CAOCCTCAGCCGTGCGGCGTCCTGGCGCGCCTGGGGGCTCCGTGCGCCTGGGGGCGCCCTCCTGCCCC
 GCGCGCCTCTGCCCCGCGCCCGCGCCCGCCCTGGCCCGGGCGCCCTGCGCGCCCGGGCTGCC
 GCACAACTGAGCTTGGAGCTGGTGGTGGCGCGCCCCCGCCCGCGAACCCGCTCGCTGACCCGC
 GGCCTGTGCCAGGCGCTGGTGCCTCCGGGCGTGGCGGCGCTGCTCGCCTTTCCCGAGGCTCGGCGCG
 AGCTGCTGCAGCTGCACTTCTGCGCGCGGCCACCGAGACCCCGTGTCTCAGCCTGCTGCGGCGGG
 AGCGCGCGCGCCCCCTCGAGCCCCGAACCCATTCCACCTGCAGCTGCACTGGGCCAGCCCCCTGG
 AGACGCTGCTGGATGTGCTGGTGGCGGTGCTGCAGGCGCACGCTGGGAAGACGTGGGCTGGCCC
 TGTGCCGCACTCAGGAACCCGCGCGCCTGGTGGCCCTCTGGAACAAGCCGGGCTGGCCCGCCCCAC
 AGCTGGTCTTGACCTAAGCGCGCGGACACGGGAGATGCAGGACTGGGGCAACGCTGGCCCCGA
 TGGCGGCGCCAGTGGGGGGTGAAGCACCGGTACCGCGCGCGCTCTCTCGGCTGTGACATCGCCC
 GTGCCCCCTCGGCTGTGGAGGCGTAACCTCCCGCGCCCCACTGGCTGTGGGGACACCACTGCGGCC
 CAAGGCCCTGCCACCGGGGCTGCCACCAGGCTGTGGCGCTGGGCGAGGTGGCAACGACCCCG
 GCTGGAGGCGCCATCCATGACATTGTGCAACTGGTGGCGGGCGCTGGGCACTGCGGCGCCAGGT
 GCAGCCGAAGCGAGCCCTCTCCCCCGCCCCGGTCAACTGGCGGGGACCTGCAGCGCGCGGGCCCCGA
 GTCCCCCGGGCGCTTCTTGGCACGTTCTTGGCCAACACGTCCTTCCAGGGCGCACGGGCGCCCGT
 TGGGTGACAGGCGCTCCCCAGACGAAGACGGGCACTGCCAGCGGGGAGCTGTGCTTGGACCCCT
 GGCACCAACGACTCGGCCAACCTGGACGCACTGTTCGCGCGCTGGCCAACGGCTCAGCGCCCCGT
 GOCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCC
 TTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCGCGCTGGACC
 GOCCTGTGCGGGACCTGTGCGCGGCGGGGCCACATGGCGGTACCCAGCTTCAGTATCAACTCC
 GCGCGCTCACAGGTGGTGGACTTCACCAGCCCCCTTCTTCTCCACCAGCCTGGGCATCATGGTGGGG
 CACGGGACACGGCTCACCCATCGGTGCTTTATGTGGCCCTGCACTGGTCCACGTGGCTGGGCGT
 TTTGGGGCCCTGCACCTCACCGCGCTCTTCTCAACGTGTACGAGTGGCGTAGCCCCCTACGGCCTC
 ACGCCACGTGGCGGCAACCGCAGCACCGTCTTCTCTACTCTCAGCCCTCAACCTGTGCTACGCCA
 TCTCTTCAGACGACCGTGTCCAGCAAGACGCCAAGTGGCCACGGGCGCGCTGCTCATGAACT
 TGGGGCATCTTCTGCTGCTGGTGTGTCCAGCTACAAGGCCAACCTGGCTGCGGTCTATGGTGGG
 JACAAGACCTTCGAGGAGCTGTGCGGGATCCAAGAACCCCAAGCTGCACCACCCGGCGCAGGGCTT
 XCGCTTCGGCACCCTGTGGGAGAGCAGCGCGGAGCGGTACATCAAGAAGAGCTTCCCCGACATGCA
 XGCACACATGGGGGCGCACAGCGCGCCCAACCGCCCCGCGCGCTGGCATGCTCAGAGCGACCC
 XCCAAGCTCAACGCTTCATCATGGACAAGTGGCTCTGACTACGAGGTCTCCATCGACGCGGAC
 XGCAAACTGCTGACCGTGGGAAAGCCCTTCGCCATTGAGGGCTATGGGATCGGACTGCCCCAGAAC
 XCGCGCTCACTCCAACCTGTCCGAGTTCATCAGCCGCTACAAGTCTCCGGCTTCATCGACCTGCT
 XACGACAAGTGGTACAAGATGGTGCCTTGGCGCAAGCGGTCTTTGCGGTTACAGAGACCTGCA
 XATGAGCATCTACCACTTCGCGGGGCTCTTGGTGTGTGCTGTGCTGGGCTGGGCGAGCGCTGCTC
 XGCTCGCTGGCGGAGCACGCTTCTTCCGCTGGCGCTGCGGCGCATCCGCAAGGGGAGCAGGCTG
 XAGTACTGGCTGCACACGAGCCAGAAAATCCACCGCGCCTCAACACGGAGCCACAGAGGGGTG
 XAGGAGGAGACGGCAGAGCGGAGGCCAGCGGCGCCCGAGGTGGAGCAGCAGCAGCAGCAGG
 XCCAGCCAACGGCTCCCGAGGGCTGGAAACGGGCGCGCGGGGCCGTGGACAAGGAGGGCGCGT
 XGCTTCTGCTGGAGCCCCCGTGGTGTGGCAACCGAAGCGGACGCGGAGGGGAGGCTGCGCG
 XGAGAGGGCCCCGTCTGGCTGTGCTCTACGCGCGCGCGCGCGCGCAAGGCCACGGGGCCCCC
 XAGCCCGGGAGCTGCAGGAGCTGGAGCGCGCATCGAAGTGGCGGTGAGCGGCTCCGCCAGGCC
 TGGTGGGGCGGGCCAGCTCTGGCACAGCTGGGGACAGCGCACGTCAACCGCTCGGCGCTT
 TTCAGGCCAGAGGGGCCCCCGGAGGGCCCCACCACTCTGGCGGACCGGGGAGCCAGGAATGA

FIG. 13

MEFVRALWLQLALALGPGSAGGHPQPCGVLARLGGSVRLGALLPRAPLARARARAALARAALAPRLPH
NLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAFPEARPELLQLHFLAAATETPVLSLLRREARAP
LGAPNPFHLQLHWASPLETLDDVLVAVLQAHAWEDVGLALCARTQDPGGLVALWTSRAGRPPQLVLDLS
RRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGCDIARARRVLEAVPPGPHWLLGTPLPPKALPTAGLP
POLLALGEVARPPLEAAIHDIQVLVARALGSAAQVQPKRALLPAPVNCGLDLPAGPESPGRFLARFLANT
SFQGRTPGVVWVGSSPDDEGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER
LAEDTPFDLFLYLVDGKYGALRDGRWTGLVGDLLAGRAHMAVTSPSINSARSQVVDFTSPFPSTSLGI
MVRARDTASPIGAFMWPLHWSTWLGVFALHLTALFLTVYEWRSPLYQLTPRGRNRSTVESYSSALNLC
YAILFRRTVSSKTPKCPTGRLLMNLWAFCLLVLSSTANLAAVMVGDKTFEELSGIHDPKLHHPAQGFR
FGTVWESSABAYIKKSFPDMHAHMRRHSAPTTPRGVAMLTSDPPKLNAFMDKSLLDYEVSIDADCKLL
TVGKFFAIEGYGIQLPQNSPLTSNLSEFISRYKSSGFIDLLHDKWYKMPVPCGKRVFAVTETLQMSIYHFAQ
LFVLLCLGLGSALLSSLGHHAFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEPSGPE
VEQQQQQQDQPTAPEGWKRARRAVDKERRVRFLLEPAVVVAPEADAEAEAAPREGPVWLCSYGRPPA
ARPTGAPOPGELQELERRIEVARERLRQALVRRGQLLAQLGDSARHRPRRLQARAAPAEAPPHSGRPGS
QE

FIG. 14

Score = 3832 (575.0 bits), Expect = 0.0, Sum P(3) = 0.0
Identities = 948/1107 (85%), Positives = 948/1107 (85%), Strand = Plus / Plus

Query: 788 CACTGCCGCCCAAGGCCCTGCCACCGCGGGCTGCCACCAGGGCTGCTGGCGCTGGGCG 847
C CTGCC CC A G C CTG CCA C CG CT CCA GC C GGC C G G G
Sbjct: 22736 CCTGCC-CCTAGGTCCTGCCCAACACGTC-CTTCCAGGGCCGCA-CGGGCCCGCTGTC 22792

Query: 848 AGGTGGCAGC-ACCCCCGCTGG-AGGCC-G-C-CATC-CATGACATTGTGCAACTGGTGG 901
GGTG CA G A C CC C GG A C G C C C C T A TGTG A C T G
Sbjct: 22793 -GGTGACAGGCAGCTCC-CAGGTACACATGTCTCGGCACTTTAAGGTGTGGAGCCT-TCG 22849

Query: 902 CCGGGCGCT-GGGCAGTGGCGGCCAGGTGCAGCCGAAGCGAGCCCTCCTCCCCGCCCCG 960
CC GG C C GCG G C G CC GG CA C G G AGC C C GCG G
Sbjct: 22850 CCGGACCCACGGGGCGCTCCCGGCTGGGCCA-CGGTGGGCAGCTGGCGGGACGGCCA-G 22907

Query: 961 GTCAACTGCCGGGACCTGCAGCCGGCCGGGCCGAGTCCCCGGGGCG-CTTCTTGGCAGC 1019
T ACT GG ACC G AG G C GC CG G CCCCC C C TG C G
Sbjct: 22908 CTGGACTT--GGAACCGGGAGGTCCCTCTGCACG-GCCCCCGCCCCACAGGGTGGCCAG 22964

Query: 1020 GTTCCTGGCC-AA-CA-CGTCTTCAGGGCCGCAAGGGC-CCCGTGTGGGTGACAGGCA 1075
GT CTGCC AA C CGT T A GC G G C CCC T TG GT G C
Sbjct: 22963 GT--CTGGCCCAAGCTGCGTG-TGTAACGCTGTTCGAACACCCATTTGTGTTT--GCCC 23019

Query: 1076 GCTCCCCAGACGAAGACGGGCAGTCCCCAGCGGGCAGCTGTCCCTGGACCCTGGCACCA 1135
G CCAGACGAAGACGGGCAQTCCCCAGCGGGCAGCTGTCCCTGGACCCTGGCACCA
Sbjct: 23020 GTGATCCAGACGAAGACGGGCAGTCCCCAGCGGGCAGCTGTCCCTGGACCCTGGCACCA 23079

Query: 1136 ACGACTCGGCCACCCCTGGACGCACTGTTCCGCCGCTGGCCAACGGCTCAGCGCCCCGTG 1195
ACGACTCGGCCACCCCTGGACGCACTGTTCCGCCGCTGGCCAACGGCTCAGCGCCCCGTG
Sbjct: 23080 ACGACTCGGCCACCCCTGGACGCACTGTTCCGCCGCTGGCCAACGGCTCAGCGCCCCGTG 23139

FIG. 14 Continued

Query: 1196 CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 1255
 CCCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA
 Sbjct: 23140 CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 23199

Query: 1256 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTTCGCGGACG 1315
 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTTCGCGGACG
 Sbjct: 23200 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTTCGCGGACG 23259

Query: 1316 GCCGCTGGACCGGCTGGTTCGGGGACCTGCTGGCCGGCCGGGCCACATGGCGGTACCA 1375
 GCCGCTGGACCGGCTGGTTCGGGGACCTGCTGGCCGGCCGGGCCACATGGCGGTACCA
 Sbjct: 23260 GCCGCTGGACCGGCTGGTTCGGGGACCTGCTGGCCGGCCGGGCCACATGGCGGTACCA 23319

Query: 1376 GCTTCAGTATCAACTCCGCCCCGCTCACAGGTGGTGGACTTCACCAGCCCCCTTCTTCTCCA 1435
 GCTTCAGTATCAACTCCGCCCCGCTCACAGGTGGTGGACTTCACCAGCCCCCTTCTTCTCCA
 Sbjct: 23320 GCTTCAGTATCAACTCCGCCCCGCTCACAGGTGGTGGACTTCACCAGCCCCCTTCTTCTCCA 23379

Query: 1436 CCAGCCTGGGCATCATGGTGCGGGCACGGGACACGGCCTCACCCATCGGTGCCTTTATGT 1495
 CCAGCCTGGGCATCATGGTGCGGGCACGGGACACGGCCTCACCCATCGGTGCCTTTATGT
 Sbjct: 23380 CCAGCCTGGGCATCATGGTGCGGGCACGGGACACGGCCTCACCCATCGGTGCCTTTATGT 23439

Query: 1496 GGCCCCCTGCACCTGGTCCACGTGGCTGGGCGTCTTTGCGGCCCTGCACCTCACCGCGCTCT 1555
 GGCCCCCTGCACCTGGTCCACGTGGCTGGGCGTCTTTGCGGCCCTGCACCTCACCGCGCTCT
 Sbjct: 23440 GGCCCCCTGCACCTGGTCCACGTGGCTGGGCGTCTTTGCGGCCCTGCACCTCACCGCGCTCT 23499

Query: 1556 TCCTCACCCTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA 1615
 TCCTCACCCTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA
 Sbjct: 23500 TCCTCACCCTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA 23559

Query: 1616 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGAGGCA 1675
 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGAGGCA
 Sbjct: 23560 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGAGGCA 23619

Query: 1676 CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGCCA 1735
 CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGCCA
 Sbjct: 23620 CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGCCA 23679

Query: 1736 TCTTCTGCCTGCTGGTGTCTGTCAGCTACACGGCCAACCTGGCTGCCGTATGGTCGGGG 1795
 TCTTCTGCCTGCTGGTGTCTGTCAGCTACACGGCCAACCTGGCTGCCGTATGGTCGGGG
 Sbjct: 23680 TCTTCTGCCTGCTGGTGTCTGTCAGCTACACGGCCAACCTGGCTGCCGTATGGTCGGGG 23739

Query: 1796 ACAAGACCTTCGAGGAGCTGTTCGGGATCCACGACCCCAAGCTGCACACC-CCGCCAG 1854
 ACAAGACCTTCGAGGAGCTGTTCGGGATCCACGACCCCAAG TG C CC CGG G G
 Sbjct: 23740 ACAAGACCTTCGAGGAGCTGTTCGGGATCCACGACCCCAAGGTGGGCGGCTCGG-G-G 23796

Query: 1855 GGCTTCCGCTTCGGCACCGTGTGGGAGAGCAAGC-CCGAGG 1894
 GGCT C G T GGC G G GGG AGC G G CC GG
 Sbjct: 23797 GGCTGCGGGT--GGCCTTGGG-GGGCTAGCGGTGGCCCCGG 23834

FIG. 15

Score = 2481 (873.4 bits), Expect = 0.0, Sum P(2) = 0.0
Identities = 469/474 (98%), Positives = 470/474 (99%), Frame = +1

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Query: 1063 WVTGSSPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 1242
      +V    PDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER
Sbjct: 427 FVFARDPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 486

Query: 1243 LAEDTPFDFFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 1422
      LAEDTPFDFFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS
Sbjct: 487 LAEDTPFDFFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 546

Query: 1423 PFFSTSLGINVRARDTASPIGAFMPLHNSTWLGVFAALHLTALFLTVEYWRSPYGLTPR 1602
      PFFSTSLGINVRARDTASPIGAFMPLHNSTWLGVFAALHLTALFLTVEYWRSPYGLTPR
Sbjct: 547 PFFSTSLGINVRARDTASPIGAFMPLHNSTWLGVFAALHLTALFLTVEYWRSPYGLTPR 606

Query: 1603 GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSSTYANLAA 1782
      GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSSTYANLAA
Sbjct: 607 GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSSTYANLAA 666

Query: 1783 VMVGDKTFEELSGIHDPKLHHPAQGFREFGTWESSAEAYIKKSFPDMHAHMRRHSAPTTP 1962
      VMVGDKTFEELSGIHDPKLHHPAQGFREFGTWESSAEAYIKKSFPDMHAHMRRHSAPTTP
Sbjct: 667 VMVGDKTFEELSGIHDPKLHHPAQGFREFGTWESSAEAYIKKSFPDMHAHMRRHSAPTTP 726

Query: 1963 RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSN 2142
      RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSN
Sbjct: 727 RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSN 786

Query: 2143 LSEFISRYKSSGFIDLLHDKWYKMVPCGKRVPFVAVTETLQMSIYHFAGLFVLLCLGLGSAL 2322
      LSEFISRYKSSGFIDLLHDKWYKMVPCGKRVPFVAVTETLQMSIYHFAGLFVLLCLGLGSAL
Sbjct: 787 LSEFISRYKSSGFIDLLHDKWYKMVPCGKRVPFVAVTETLQMSIYHFAGLFVLLCLGLGSAL 846

Query: 2323 LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEAP 2484
      LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEAP
Sbjct: 847 LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEAP 900

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24/48

[illegible]

25/48

ATGGAGTTTGTGCGGGCGCTGTGGCTGGGCTGGCGCTGGCGCTGGGGCGGGGTCCGGCGGGGGG
CACCTCAGCGTGC GGCGTCTTGGCGCGCTCGGGGGCTCCGTGGCGCTGGGC0CCTCCTGCCCC
GCGCGCTCTCGCCCGCGCCCGCGCCCGCGCGCGCTGGCCCGGGCGCCCTGGCGCGCGGCTGCC
GCACAACCTGAGCTTGGAGCTGGTGTGTGGCGCGCCCGCGCCCGCGCGA0CCCGCTCGCTGACCCG
GGCTGTGCCAGGCGCTGTGTCTCGGGCGGTGGCGCGCCCGCGCGCGA0CCCGCTCGCTGACCCG
AGCTGCTGCAGCTGCACCTTCTTGGCGCGCGGCCACCGAGACCCCGTGTCTAGCCTGTGTGGGGGG
AGGCGCGCGCGCCCTCGGAGCCCCGAACCCATTCCACCTGCAGCTGCACTGGGCCAGCC0CCTGG
AGACGCTGCTGGATGTCTGGTGGCGGTGCTGCA0GCGACGCTGGGAAGACGTTCGGCTGGCC
TGTGCCGCACTCAGGACCCCGGCGCGCTGGTGGCCCTCTGGAACAAGCCGGGTGGCCGGCCCCAC
AGCTGGTCTGGACCTAAGCCGGCGGGACACGGGAGATGCAGGACTGCGGGCA0CCTGGCCCGGA
TGGCGCGGCCA0TGGGGGTGAAGCA0CGTACCCGCGCGGTCTCTCGCTGTGACATCCCC
GTGCCGTTCGGGTGCTGGAGGCGTACCTCCCGCCCCCACTGGCTGTGGGGACACCACTGCCCG
CAAGGCCCTGCCACCGCGGGGTGCCACCA0GGGTGCTGGCGTGGGCGA0GTGGCAGCA0CCCG
GCTGGAGGCGGCATCCATGACATTGTGCAACTGGTGGCCCGGGCGCTGGCAGTGGCC0CAGGT
GCAGCGAAGCGAGCCCTCCTCCCCGCCCCGGTCAACTGGCGGACCTGTCAGCGCGCGGGGCCGA
GTCCCCGGGGCGCTTCTTGGCACGGTCTCTGGCCAACACGTCTTCCAGGGCCGCACGGG0CCGT
TGGGTGACAGGCAGCTCC0AGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCGGGACC
CACGGGGCGCCCCGGCTCGCCCA0GTGGCAGCTGGCGGACGGCCAGCTG0ACTTGGAA0CGG
GAGGTGCCTCTGCACCGCTCCCCCGCCCCCA0GGGTGCCAGGTCTGGCCAAAGCTGGTGTGTAA
CGCTGTTGGAAAC0CATTTGTGTTTGGCCGTGATCCAGACGAAGA0GGGCAGTGCCAGCGGGG
AGCTGTGCTGGA0CCTGGCA0CA0GACTCGGCCACCTGGA0GCACTGTTCGCGCGCTGGCCAA
CGCTCAGCGCCCCGTGCCCTGCGCA0GTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGT
GCGGAGGACACGCGCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCG0CTGCG
GACGGCGCTGGAC0GGCCTGTTCGGGGACCTGCTGGCCGGCGGGGCCACATGGCGGTACCCAG
TTCAGTATCAACTCCG0CGCTCACAGGTGGTGGACTTCACCA0CCCTTCTTCCACCA0CCTGG
GCATCATGGTGGGGGACGGGACACGGCCTCA0CATCGGTGCTTTATGTGG0CCTGCACTGGT
CACGTGGCTGGGCGTCTTTGGCGCCTGCACCTCA0CGCGCTCTCTCCTAC0GTGACGAGTGGGT
AGCCCTACGGCCTACGGCA0GTGGCCGCA0CCGACGACCGCTTCTCCTACTCCTCAGCCCTCA
ACCTGTGTACGCCATCCTCTTCAGACGCA0GTGTCCAGCAAGACGCCCAAGTGGCCACGGGCG
CCTGCTCAT0A0CTTGGGCCATCTTCTGCTGTGGTGTGTGCTGTCCAGCTACACGGCA0CCTGGCT
GCCGTATGGTGGGGACAAGACCTTCGAG0AGCTGTGGGGATCCA0GACCCCAAGCTGCA0CAC
CCGGGACAGGGCTTCGCTTCGGCACCGTGTGGGAGAGCAGCGCCGAGGCGTACATCAAGAAGAGC
TTCCCGCATGACACGCA0CATGGCGGCCACAGCGCGCCACCA0CGCCCGCGCGGTGGCATG
CTCACGAGCGA0CC0CCAAGCTCAAC0CCTTCATCATGGACAAGTCTGCTCCTGGACTACGAGGTCT
CCATOGACGCG0ACTGCAAACTGCTGACCGTGGGAAAGCCCTTCGCCATTGAGGGCTATGGGATG
GACTGCCCCAGAACTGCGCGCTCACCTCCA0CCTGTCCGAGTTCATCAGCCGCTACAAGTCTCCG
CTTCATCGA0CTGCTCCACGACAAGTGGTACAAGATGGTGCCTTGGGCAAGCGGGTCTTTGGCGTT
ACAGAGACCTGCAGATGAGCATCTACCACTTCGCGGGCCTCTTCTGTGTGCTGTGCTGGCCTGGCG
GCAGGCTCTGCTCAGCTCGCTGGGCGAGCACGCTTCTTCGCTGGCGCTGGCGCTGACATCCGAA
GGGGAGCAGGCTGCACTACTGGCTGCACACAGCCAGAAAATCACCGCGCCTCAACACGAGGCC
ACCAGAGGGGTGGAAGGAG0AGACGGCAGAGGGGAGCCACGGCCCCGAGGTGGAGCAGCAGC
AGCAGCAGCAGGACCAG0CA0CGCTCCGCGAGGGCTGGAAACGCGGCGCGCGGGGCGGTGGACAAG
GAGCGCGCGTTCGCTTCTGCTGGAGCGCGCGGTGTGTGTGGCACCCGAAGCGGACCGGAGGGG
GAGGCTGCGCGCGA0GGCCCCGTCTGGCTGTGCTCCTACGGCCGCGCGCCCGCGCAAGGCC
ACGGGGGCCCCCAGCCCGGGGAGCTGACAGAGCTGGAGCGCGCATCGAAGTCCGCGGTGAGCG
GCTCCGCGAGGCCCTGTGCGGCGCGGOCAGCTCTGGCACAGCTCGGGGACAGCGCA0GTACCG
GCTCGCGCTTGCTTACGGOCAGAGCGGCCCCCCCGGAGGCCCA0CA0ACTCTGGCCGACCGG
GAGCCAGGAATGA

FIG. 18

MEFVRALWLGLALALGPGSAGGHPQPCGVLARLGGSVRLGALLPRAPLARARARAALARAALAPRLPH
NLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAPPEARPELLQLHFLAAATETPVLSLLRREARAP
LGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTQDPGGLVALWTSRAGRPPQLVLDLS
RRDTGDAGLRARLAPMAAPVCGEAPVPAAVLLGCDIARARRVLEAVPPGPHWLLGTPLPPKALPTAGLP
PGLLALGEVARPPLEAAIHDIQVVARALGSAAQVQPKRALLPAPVNCGLQAPGPESPGRFLARFLANT
SFQGRTPGVVWTGSSQVHMSRHFVWVSLRRDPRGAPAWATVGSWRDQQLDLEPGGASARPPPPQGAQ
VWPKLRVVTLLEHPFVFARDPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKOCYGYCI
DLLERLAEDTPFDLFELYLVGDKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTSPFFS
TSLGIMVRARDTASPIGAFMWPLHWSTWLGVFALHLTALFLTVEWRSPYGLTPGRNRSTVFSYSSA
LNLGYAILFRRTVSSKTPKCPTGRLLMNLWAFCLLVLSYTNLAAMVVGDKTFEELSGIHDPKLHHPA
QGFRPGTVWESSAEAYIKKSFPDMHAHMRRHSAPTTPRGVAMLTSDPPKLNAFIMDKSLLDYEVSIDAD
CKLLTVGKPFATIEGYGIGLPQNSPLTSNLSEFISRYKSSGFIDLLHDKWYKMPCKRVFAVTETLQMSIY
HFAGLFVLLCLGLGSALLSSLGEHAFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKERTAEAEF
SGPEVEQQQQQDQPTAPEGWKRARRAVDKERRVRFLEPAVVVAPEADAEAEAAAPREGPVWLC SYG
RPPAARPTGAPQPGELQELERRIEVARERLRQALVRRGQLLAQLGDSARHRPRRLQARAAPAEAPPHSG
RPGSQE

FIG. 19

Score = 5188 (778.4 bits), Expect = 0.0, Sum P(4) = 0.0
Identities = 1068/1092 (97%), Positives = 1068/1092 (97%), Strand = Plus / Plus

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Query:  1019  GGTTCCTGGCCAAACACGTCCTTCCAGGGCCGCACGGGCCCCGTGTGGGTGACAGGCAGCT  1078
           GGTTCCTGGCCAAACACGTCCTTCCAGGGCCGCACGGGCCCCGTGTGGGTGACAGGCAGCT
Sbjct:  22747 GGTTCCTGGCCAAACACGTCCTTCCAGGGCCGCACGGGCCCCGTGTGGGTGACAGGCAGCT  22806

Query:  1079  CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCCGGGACCCACGGGGCG  1138
           CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCCGGGACCCACGGGGCG
Sbjct:  22807 CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCCGGGACCCACGGGGCG  22866

Query:  1139  CCCCCGCCCTGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGGAACCGGGAG  1198
           CCCCCGCCCTGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGGAACCGGGAG
Sbjct:  22867 CCCCCGCCCTGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGGAACCGGGAG  22926

Query:  1199  GTGCCTCTGCACGGCCCCCGCCCCACAGGGTGCCAGGTCTGCCCCAAGCTGCCGTGTGG  1258
           GTGCCTCTGCACGGCCCCCGCCCCACAGGGTGCCAGGTCTGCCCCAAGCTGCCGTGTGG
Sbjct:  22927 GTGCCTCTGCACGGCCCCCGCCCCACAGGGTGCCAGGTCTGCCCCAAGCTGCCGTGTGG  22986

Query:  1259  TAACGCTGTTGGAACACCCATTGTGTTTGCCCGTGATCCAGACGAAGACGGGCAGTGCC  1318
           TAACGCTGTTGGAACACCCATTGTGTTTGCCCGTGATCCAGACGAAGACGGGCAGTGCC
Sbjct:  22987 TAACGCTGTTGGAACACCCATTGTGTTTGCCCGTGATCCAGACGAAGACGGGCAGTGCC  23046

Query:  1319  CAGCGGGGCAGCTGTGCCCTGGACCCCTGGCACCAACGACTCGGCCACCCTGGACGCACTGT  1378
           CAGCGGGGCAGCTGTGCCCTGGACCCCTGGCACCAACGACTCGGCCACCCTGGACGCACTGT
Sbjct:  23047 CAGCGGGGCAGCTGTGCCCTGGACCCCTGGCACCAACGACTCGGCCACCCTGGACGCACTGT  23106

Query:  1379  TCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTGCCCTGCGCAAGTGCTGCTACGGCTACT  1438
           TCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTGCCCTGCGCAAGTGCTGCTACGGCTACT
Sbjct:  23107 TCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTGCCCTGCGCAAGTGCTGCTACGGCTACT  23166

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FIG. 19 Continued

Query: 1439 GCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG 1498
 GCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG
 Sbjct: 23167 GCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG 23226

Query: 1499 TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCGCTGGACCGGCTGGTCGGGGACC 1558
 TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCGCTGGACCGGCTGGTCGGGGACC
 Sbjct: 23227 TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCGCTGGACCGGCTGGTCGGGGACC 23286

Query: 1559 TGCTGGCCGGCCGGGCCACATGGCGGTACACAGCTTCAGTATCAACTCCGCCCGCTCAC 1618
 TGCTGGCCGGCCGGGCCACATGGCGGTACACAGCTTCAGTATCAACTCCGCCCGCTCAC
 Sbjct: 23287 TGCTGGCCGGCCGGGCCACATGGCGGTACACAGCTTCAGTATCAACTCCGCCCGCTCAC 23346

Query: 1619 AGGTGGTGGACTTCACCAGCCCCCTCTTCTCCACCAGCCTGGGCATCATGGTGGGGCAC 1678
 AGGTGGTGGACTTCACCAGCCCCCTCTTCTCCACCAGCCTGGGCATCATGGTGGGGCAC
 Sbjct: 23347 AGGTGGTGGACTTCACCAGCCCCCTCTTCTCCACCAGCCTGGGCATCATGGTGGGGCAC 23406

Query: 1679 GGGACACGGCCTCACCCATCGGTGCCCTTATGTGGCCCTGCACCTGGTCCACGTGGCTGG 1738
 GGGACACGGCCTCACCCATCGGTGCCCTTATGTGGCCCTGCACCTGGTCCACGTGGCTGG
 Sbjct: 23407 GGGACACGGCCTCACCCATCGGTGCCCTTATGTGGCCCTGCACCTGGTCCACGTGGCTGG 23466

Query: 1739 GCGTCTTTGCGGCCCTGCACCTCACCGCGCTCTTCTCACCCTGTACGAGTGGCGTAGCC 1798
 GCGTCTTTGCGGCCCTGCACCTCACCGCGCTCTTCTCACCCTGTACGAGTGGCGTAGCC
 Sbjct: 23467 GCGTCTTTGCGGCCCTGCACCTCACCGCGCTCTTCTCACCCTGTACGAGTGGCGTAGCC 23526

Query: 1799 CCTACGGCCTCACGCCACGTGGCCGCAACCGCAGCACCCTCTTCTCCTACTCCTCAGCCC 1858
 CCTACGGCCTCACGCCACGTGGCCGCAACCGCAGCACCCTCTTCTCCTACTCCTCAGCCC
 Sbjct: 23527 CCTACGGCCTCACGCCACGTGGCCGCAACCGCAGCACCCTCTTCTCCTACTCCTCAGCCC 23586

Query: 1859 TCAACCTGTGCTACGCCATCCTCTTCAGACGCACCCTGTCCAGCAAGACGCCCAAGTGCC 1918
 TCAACCTGTGCTACGCCATCCTCTTCAGACGCACCCTGTCCAGCAAGACGCCCAAGTGCC
 Sbjct: 23587 TCAACCTGTGCTACGCCATCCTCTTCAGACGCACCCTGTCCAGCAAGACGCCCAAGTGCC 23646

Query: 1919 CCACGGCCCGCCTGCTCATGAACCTCTGGGCCATCTTCTGCCTGCTGGTGTGTCCAGCT 1978
 CCACGGCCCGCCTGCTCATGAACCTCTGGGCCATCTTCTGCCTGCTGGTGTGTCCAGCT
 Sbjct: 23647 CCACGGCCCGCCTGCTCATGAACCTCTGGGCCATCTTCTGCCTGCTGGTGTGTCCAGCT 23706

Query: 1979 ACACGGCCAACCTGGCTGCCGTCATGGTGGGGACAAGACCTTCGAGGAGCTGTGGGGA 2038
 ACACGGCCAACCTGGCTGCCGTCATGGTGGGGACAAGACCTTCGAGGAGCTGTGGGGA
 Sbjct: 23707 ACACGGCCAACCTGGCTGCCGTCATGGTGGGGACAAGACCTTCGAGGAGCTGTGGGGA 23766

Query: 2039 TCCACGACCCCAAGCTGCACCACC-CGCGCAGGGCTTCGCTTCGGCACCGTGTGGGAG 2097
 TCCACGACCCCAAG TG C CC CGG G GGGCT C G T GGC G G GGG
 Sbjct: 23767 TCCACGACCCCAAGGTGGCGGGCTCGG-G--GGGCTGCGGT--GGCCTTGGG-GGGCT 23820

Query: 2098 AGCAGCG-CCGAGG 2110
 AGC G G CC GG
 Sbjct: 23821 AGCGGTGGCCCCGG 23834

FIG. 20

Score = 4730 (1665.0 bits), Expect = 0.0, P = 0.0

Identities = 900/900 (100%), Positives = 900/900 (100%), Frame = +1

Query: 1 MEFVRAIMLGLALALGPGSAGGHPQPCGVLARLGGSVRLGALLPRAFLARARARAALARA 180
MEFVRAIMLGLALALGPGSAGGHPQPCGVLARLGGSVRLGALLPRAFLARARARAALARA
Sbjct: 1 MEFVRAIMLGLALALGPGSAGGHPQPCGVLARLGGSVRLGALLPRAFLARARARAALARA 60

Query: 181 ALAPRLPHNLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAPPEARPELLQLHFLA 360
ALAPRLPHNLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAPPEARPELLQLHFLA
Sbjct: 61 ALAPRLPHNLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAPPEARPELLQLHFLA 120

Query: 361 AATETPVLSLLRREARAPLGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCR 540
AATETPVLSLLRREARAPLGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCR
Sbjct: 121 AATETPVLSLLRREARAPLGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCR 180

Query: 541 TQDPGGLVALWTSRAGRPPQLVLDLSRRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGC 720
TQDPGGLVALWTSRAGRPPQLVLDLSRRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGC
Sbjct: 181 TQDPGGLVALWTSRAGRPPQLVLDLSRRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGC 240

Query: 721 DIARARRVLEAVFPGPHWLLGTPLPPKALPTAGLPPGILLALGEVARPFLAAIHDIQVLV 900
DIARARRVLEAVFPGPHWLLGTPLPPKALPTAGLPPGILLALGEVARPFLAAIHDIQVLV
Sbjct: 241 DIARARRVLEAVFPGPHWLLGTPLPPKALPTAGLPPGILLALGEVARPFLAAIHDIQVLV 300

Query: 901 ARALGSAAQVQPKRALLPAPVNCGLQAGPESPGRFLARFLANTSFOGRTGPFVWVTGSS 1080
ARALGSAAQVQPKRALLPAPVNCGLQAGPESPGRFLARFLANTSFOGRTGPFVWVTGSS
Sbjct: 301 ARALGSAAQVQPKRALLPAPVNCGLQAGPESPGRFLARFLANTSFOGRTGPFVWVTGSS 360

Query: 1081 QVHMSRHFVWLSLRRDPRGAPAWATVGSWRDQQLDLEPGGASARPPPPQGAQVWPCLRUV 1260
QVHMSRHFVWLSLRRDPRGAPAWATVGSWRDQQLDLEPGGASARPPPPQGAQVWPCLRUV
Sbjct: 361 QVHMSRHFVWLSLRRDPRGAPAWATVGSWRDQQLDLEPGGASARPPPPQGAQVWPCLRUV 420

Query: 1261 TLLEHPFVFARDPDEDGQCQAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYC 1440
TLLEHPFVFARDPDEDGQCQAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYC
Sbjct: 421 TLLEHPFVFARDPDEDGQCQAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYC 480

Query: 1441 IDLLERLAEDTPFDFFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSO 1620
IDLLERLAEDTPFDFFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSO
Sbjct: 481 IDLLERLAEDTPFDFFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSO 540

FIG. 20 Continued

Query: 1621 VVDFTSPFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFALHLTALFLTVYENRSP 1800
VVDFTSPFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFALHLTALFLTVYENRSP
Sbjct: 541 VVDFTSPFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFALHLTALFLTVYENRSP 600

Query: 1801 YGLTFRGRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSY 1980
YGLTFRGRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSY
Sbjct: 601 YGLTFRGRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSY 660

Query: 1981 TANLAAMVGDKTFEELSGIHDPKLHHPAQGFRTVWESSAEAYIKKSFFDMHAMRRH 2160
TANLAAMVGDKTFEELSGIHDPKLHHPAQGFRTVWESSAEAYIKKSFFDMHAMRRH
Sbjct: 661 TANLAAMVGDKTFEELSGIHDPKLHHPAQGFRTVWESSAEAYIKKSFFDMHAMRRH 720

Query: 2161 SAPTTFRGVAML/TSDFPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQN 2340
SAPTTFRGVAML/TSDFPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQN
Sbjct: 721 SAPTTFRGVAML/TSDFPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQN 780

Query: 2341 SPLTSNLSEFISRYKSSGFIDLLHDKWYKMVPCGKRVFVAVTETLQMSIYHFAGLFVLLCL 2520
SPLTSNLSEFISRYKSSGFIDLLHDKWYKMVPCGKRVFVAVTETLQMSIYHFAGLFVLLCL
Sbjct: 781 SPLTSNLSEFISRYKSSGFIDLLHDKWYKMVPCGKRVFVAVTETLQMSIYHFAGLFVLLCL 840

Query: 2521 GLGSALLSSLGEHAFFRLALPRIKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEBEP 2700
GLGSALLSSLGEHAFFRLALPRIKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEBEP
Sbjct: 841 GLGSALLSSLGEHAFFRLALPRIKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEBEP 900

FIG. 21

Glutamate_Receptor_RAT_AAD4165
Glutamate_Receptor_Human_06039
21659259_IDCT3

RRRSLWVLSRMCLLDPFCALVLAQVSSSSHPQPCQSKKCHAVFAGAGHLQPVTT
MEFVRALWLG--LALALGF-----SS--AGGHPPQPCGVLAELGGSVRLGALLPF....
MEFVRALWLG--LALALGF-----SS--AGGHPPQPCGVLAELGGSVRLGALLPF....

Glutamate_Receptor_RAT_AAD4165
Glutamate_Receptor_Human_06039
21659259_IDCT3

APRFASEAQEGGFAAAQDDPESGTWRPPAPSQARWLQSLHGFQPPGSRKLGGAGAG
APLARARA....PAALAE-----AALAPE-----
APLARARA....PAALAE-----AALAPE-----

Glutamate_Receptor_RAT_AAD4165
Glutamate_Receptor_Human_06039
21659259_IDCT3

YLWPRDALLFAVENLNRVEGLFYHLSLELVAIAEALODLPLMPFSSPSPWSSDFFV
-----LPHNLSLELVVAAPP-----ADDPASL
-----LPHNLSLELVVAAPP-----ADDPASL

Glutamate_Receptor_RAT_AAD4165
Glutamate_Receptor_Human_06039
21659259_IDCT3

LQSGHTGVVGVSAALLAFQSQGEMICDLSSVLHIVLSHSEEF--PRESQGLH
TRGLCCALVPPGVAALLAFPEARPELLQLHFLAAATETPVLSLRREARAPLGADNPFIL
TRGLCCALVPPGVAALLAFPEARPELLQLHFLAAATETPVLSLRREARAPLGADNPFIL

Glutamate_Receptor_RAT_AAD4165
Glutamate_Receptor_Human_06039
21659259_IDCT3

QLSLENSLSADAVTSLELTMNNYNFSLCCQEDWNITDFLLTENNSEKFELESVENH
QLHWASPLETLDDVLVAVLQAHAWEDVGLALCRTQDPGGGLVALWTSFAG--RPPQLVIDLS
QLHWASPLETLDDVLVAVLQAHAWEDVGLALCRTQDPGGGLVALWTSFAG--RPPQLVIDLS

Glutamate_Receptor_RAT_AAD4165
Glutamate_Receptor_Human_06039
21659259_IDCT3

ANLSTKDELSTFLQVQMDNIR--NSTFTLCTCCDDDSIQPFEMSTQFGSPPELHML
RSDTGDAGLFAELAPMAAPVGGGAAPVPAAVLLGCCIAAPAEVLEA-----VPPGPHML
RSDTGDAGLFAELAPMAAPVGGGAAPVPAAVLLGCCIAAPAEVLEA-----VPPGPHML

Glutamate_Receptor_RAT_AAD4165
Glutamate_Receptor_Human_06039
21659259_IDCT3

EDSONVKEERLEBLLELMAHUKTYQSVFYHQDAELVARANNDTMTNFKALLFT
STPLPPHALPTAGLPPGLLALGEVARPPLEAAIHDIVOLVARALGSAAGVQPHFALLPAT
STPLPPHALPTAGLPPGLLALGEVARPPLEAAIHDIVOLVARALGSAAGVQPHFALLPAT

Glutamate_Receptor_RAT_AAD4165
Glutamate_Receptor_Human_06039
21659259_IDCT3

ENCMQKTYN-LHSQELSEFLANTFFRLSSSKVKSTIISSENNFQANQHPMK
VNCGLDLPAGPESPGFRLARFLANTSFQGETCPVWVVGSSQVHMSHFWWGLREDDFGA
VNCGLDLPAGPESPGFRLARFLANTSFQGETCPVWVVGSSQVHMSHFWWGLREDDFGA

Glutamate_Receptor_RAT_AAD4165
Glutamate_Receptor_Human_06039
21659259_IDCT3

PLMSTRSSWQGRVVDLSIWFQAQPKTHFOHPNKLHLRVVTLLEHPFVFTLVVHSG
PAWATVGSWFDGOLDLEFG---GASARPPPPQGAQVWZHLRVVTLLEHPFVFAEDPDEG
PAWATVGSWFDGOLDLEFG---GASARPPPPQGAQVWZHLRVVTLLEHPFVFAEDPDEG

Glutamate_Receptor_RAT_AAD4165
Glutamate_Receptor_Human_06039
21659259_IDCT3

LCPAGQLCLDPTNDSMSMLDRFSSSHSSNDVPIKTECCCYGYCIDLLERLAEDTPFDF
QCPAGQLCLDPTNDSATLDALFAALANG--SAPRALRECCYGYCIDLLERLAEDTPFDF
QCPAGQLCLDPTNDSATLDALFAALANG--SAPRALRECCYGYCIDLLERLAEDTPFDF

Glutamate_Receptor_RAT_AAD4165
Glutamate_Receptor_Human_06039
21659259_IDCT3

ELYLVGDGHYGAWANGHWTCGLVCDLLSTIANMAVTSFSINSARSQVVDFTSPFFSTSLGI
ELYLVGDGHYGALEDGRWTGLVCDLLAGRAHMAVTSFSINSARSQVVDFTSPFFSTSLGI
ELYLVGDGHYGALEDGRWTGLVCDLLAGRAHMAVTSFSINSARSQVVDFTSPFFSTSLGI

FIG. 22

21659259_EXT_3	MEFVKALWGLALALGPGSAGGHPPQCGVLARKLGGSVRKLGALLPRAPLARAKARAALARA
21659259_EXT_2	MEFVKALWGLALALGPGSAGGHPPQCGVLARKLGGSVRKLGALLPRAPLARAKARAALARA
21659259_EXT_1	MEFVKALWGLALALGPGSAGGHPPQCGVLARKLGGSVRKLGALLPRAPLARAKARAALARA
21659259_EXT_3	ALAPRLPHNLSELEVAAPPARDPASLTRGLGQALVPPGVAALLAFPEARPELLOLHFLA
21659259_EXT_2	ALAPRLPHNLSELEVAAPPARDPASLTRGLGQALVPPGVAALLAFPEARPELLOLHFLA
21659259_EXT_1	ALAPRLPHNLSELEVAAPPARDPASLTRGLGQALVPPGVAALLAFPEARPELLOLHFLA
21659259_EXT_3	AATETPVLSLRRKRAKAPLGAPNPHLQLHWA SPLETLDVLVAVLQAHAWEDVGLALCR
21659259_EXT_2	AATETPVLSLRRKRAKAPLGAPNPHLQLHWA SPLETLDVLVAVLQAHAWEDVGLALCR
21659259_EXT_1	AATETPVLSLRRKRAKAPLGAPNPHLQLHWA SPLETLDVLVAVLQAHAWEDVGLALCR
21659259_EXT_3	TQDPGGGLVALWTSRAGRPPQLVLDLSKRD TGDAGLRAKLAPMAAPVGGEA PVA AVL LGC
21659259_EXT_2	TQDPGGGLVALWTSRAGRPPQLVLDLSKRD TGDAGLRAKLAPMAAPVGGEA PVA AVL LGC
21659259_EXT_1	TQDPGGGLVALWTSRAGRPPQLVLDLSKRD TGDAGLRAKLAPMAAPVGGEA PVA AVL LGC
21659259_EXT_3	DIARARRVLEAVPPGPHWLLGTPLPKALPTAGLPGLLALGEVARPPLEVAIHDI VQLV
21659259_EXT_2	DIARARRVLEAVPPGPHWLLGTPLPKALPTAGLPGLLALGEVARPPLEVAIHDI VQLV
21659259_EXT_1	DIARARRVLEAVPPGPHWLLGTPLPKALPTAGLPGLLALGEVARPPLEVAIHDI VQLV
21659259_EXT_3	ARALGSAAQVQPKRALLPAPVNGGDLQPA GPE SPGRFLARFLANTSFQGR TG P VVVTGSS
21659259_EXT_2	ARALGSAAQVQPKRALLPAPVNGGDLQPA GPE SPGRFLARFLANTSFQGR TG P VVVTGSS
21659259_EXT_1	ARALGSAAQVQPKRALLPAPVNGGDLQPA GPE SPGRFLARFLANTSFQGR TG P VVVTGSS
21659259_EXT_3	QVHMSRHF K VWSLRDP RGA P A WATVGSWRD GQLDLE P GGA SAKRPPPOGAQVWP KLRV
21659259_EXT_2	QVHMSRHF K VWSLRDP RGA P A WATVGSWRD GQLDLE P GGA SAKRPPPOGAQVWP KLRV
21659259_EXT_1	QVHMSRHF K VWSLRDP RGA P A WATVGSWRD GQLDLE P GGA SAKRPPPOGAQVWP KLRV
21659259_EXT_3	T L L E H P F V F A R D P D E D G Q C P A G O L G L D P G T N D S A T I D A L F A A L A N G S A P R A L R K C C Y G Y C
21659259_EXT_2	T L L E H P F V F A R D P D E D G Q C P A G O L G L D P G T N D S A T I D A L F A A L A N G S A P R A L R K C C Y G Y C
21659259_EXT_1	T L L E H P F V F A R D P D E D G Q C P A G O L G L D P G T N D S A T I D A L F A A L A N G S A P R A L R K C C Y G Y C

FIG. 22 Continued

21659259_EXT_3	RLLQARAAPAEAPP HSGRPGSQE
21659259_EXT_2	RLLQARAAPAEAPP HSGRPGSQE
21659259_EXT_1	RLLQARAAPAEAPP HSGRPGSQE

FIG. 23

ACGCGTTACTCCTACCAGGTTGTAGCATGCATCTTTTTGAGAGAGCAGCTGGGATCGAGTA
TACTCTTGACTTAAATATGTTTGTITTATAAAGACAAATGGAGAAATCAATTTTTTCCCTGA
ATTCTTAGGAGCACTTTAGTGAATAAAGAACCTGACAGTATGCTGGCCACATGTTTAAGG
ACAAAGGTGTCTGGGGAAATAAGCAAGATCATAGAGGAGCTTTCTTAATTGACCGAAGTCC
TGAGTACTTCGAACCCATTTTGAACACTTTCGTCATGGACAGCTCATTGTAAATGATGGCA
TTAATTTATTGGGTGTGTTAGAAGAAGCAAGATTTTTTGGTATTGACTCATTGATTGAACAC
CTAGAAGTGGCAATAAAGAATTCTCAACCACCGGAGGATCATTACCAATATCCCGAAAGG
AATTTGTCCGATTTTTGCTAGCAACTCCAACCAAGTCAGAACTGCGATGCCAGGGTTTGAA
CTTCAGTGGTGCTGATCTTTCTCGTTTGGACCTTCGATACATTAACCTTCAAAATGGCCAATT
TAAGCCGCTGTAATCTTGACATGCAAATCTTTGCTGTGCAAATCTTGAACGAGCTGATCTC
TCTGGATCAGTGCTTGACTGTGCGAATCTCCAGGGAGTCAAGATGCTCTGTTCTAATGCAG
AAGGAGCATCCCTGAAACTGTGTAATTTTGAGGATCCTTCTGGTCTTAAAGCCAATTTAGA
AGGTGCTAATCTGAAAGGTGTGGATATGGAAGGAAGTCAGATGACAGGAATTAACCTGAG
AGTGGCTACCTTAAAAAATGCAAAGTTGAAGAACTGTAACCTCAGAGGAGCAACTCTGGC
AGGAACTGATTTAGAGAATTGTGATCTGTCTGGGTGTGATCTTCAAGAAGCCAACCTGAGA
GGGTCCAACGTGAAGGGAGCTATATTTGAAGAGATGCTGACACCACTACACATGTCACAAA
GTGTCAGATGAGAATTTTAGGGGCTGGAGGAAGATGTAAAAGATGAAAATGTTTTCTTAT
CACTTTTCTTTCTCCACCCACTCAGTTGTCTAGAAGAAATAACACTGTAAGGAAATTTAAAA
AAAAAAA

FIG. 24

**MLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGINLLGVLEEARFFGID
SLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELRCQGLNFSGADLSRLDLRYINFKMAN
LSRCNLAHANLCCANLERADLSGSVLDGANLQGVKMLCSNAEGASLKLCNFEDPSGLKANLE
GANLKGVDMEGSQMTGINLRVATLKNKLCNLRGATLAGTDLENCDSLGCDDLQEANLRGS
NVKGAIFFEMLTPLHMSQSVR**

FIG. 25

Score = 1486 (523.1 bits), Expect = 1.4e-151, P = 1.4e-151
Identities = 286/286 (100%), Positives = 286/286 (100%), Frame
= +1

```
Query:   130 RSTLVNKEPDSMLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGI 309
          RSTLVNKEPDSMLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGI
Sbjct:   104 RSTLVNKEPDSMLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGI 163

Query:   310 NLLGVLEEARFFGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLLATPTKSELRCQGL 489
          NLLGVLEEARFFGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLLATPTKSELRCQGL
Sbjct:   164 NLLGVLEEARFFGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLLATPTKSELRCQGL 223

Query:   490 NPSGADLSRLDLRYINFKMANLSRCNLAHANLCCANLERADLSGGSVLD CANLQGVKMLCS 669
          NPSGADLSRLDLRYINFKMANLSRCNLAHANLCCANLERADLSGGSVLD CANLQGVKMLCS
Sbjct:   224 NPSGADLSRLDLRYINFKMANLSRCNLAHANLCCANLERADLSGGSVLD CANLQGVKMLCS 283

Query:   670 NAEGASLKL CNFEDPSGLKANLEGANLKGVDMEGSQMTGINLRVATLKNAKLNKCNLRGA 849
          NAEGASLKL CNFEDPSGLKANLEGANLKGVDMEGSQMTGINLRVATLKNAKLNKCNLRGA
Sbjct:   284 NAEGASLKL CNFEDPSGLKANLEGANLKGVDMEGSQMTGINLRVATLKNAKLNKCNLRGA 343

Query:   850 TLAGTDLENCDSLGC DLQEANLRGSGNVKGAI FEEMLTPLHMSQSVR 987
          TLAGTDLENCDSLGC DLQEANLRGSGNVKGAI FEEMLTPLHMSQSVR
Sbjct:   344 TLAGTDLENCDSLGC DLQEANLRGSGNVKGAI FEEMLTPLHMSQSVR 389
```

FIG. 26

TTTCAGGGTTCTAGCCTGTTTCATCTAGCCCCATGATGGCTGTGGACATCGAGTACAGATACAACATGCAT
GGCTCCTTCCTTGCGCCAAGAGAGGTTTGCCCTTAAAGATCTCACCAAAGCCCAGCAAACCACTGAGGCCT
TGTATTCAGCTGAGCAGCAAGAATGAAGCCAGTGGAATGGTGGCCCCGGCTGTCCAGGAGAAGAAGGTGA
AAAAGCGGGTGTCCCTTCGCAGACAACCAGGGGCTGGCCCTGACAATGGTCAAAGTGTTCGGAATTCGA
TGACCCGCTAGATATGCCATTCAACATCACCGAGCTCCTAGACAACATTGTGAGCTTGACGACAGCAGAG
AGCGAGAGCTTTGTTCTGGATTTTCCAGCCCTCTGCAGATTACTTAGACTTTAGAAATCGACTTCAGG
CCGACCACGTCTGCCTTGAGAACTGTGTGCTCAAGGACAAGGCCATTGCAGGCACGTGTGAAGGTTCAGAA
CCTCGCATTTGAGAAGACCGTGAAAATAAGGATGACGTTGACACCTGGAAGAGCTACACAGACTTTCCT
TGTCAGTACGTGAAGGACACTTATGCCGGTTCAGACAGGGACACGTTCTCCTTCGACATCAGCTTGCCCG
AGAAGATTGAGTCTTATGAAAGAATGGAGTTTGCTGTGTACTACGAGTGCAATGGACAGACGTACTGGGA
CAGCAACAGAGGCAAGAAGCTATAGGATCATCCGGGCTGAGTTAAATCTACCCAGGGAATGACCAAGCCC
CACAGTGGACCGGATTTGGGAATATCCTTTGACCAGTTCGGAAGCCCTCGGTGTTCTATGGTCTGTTTC
CAGAGTGGCCAAGTTACTTAGGATATGAAAAGCTAGGGCCCTACTACTAGTGACTGCAGGTGACAGGGCG
TGGCGGAGCTGCCACA

FIG. 27

**MMAVDIEYRYNCMAPSLRQERFAFKISPKPSKPLRPCIQLSSKNEASGMVAPAVQEKKVKKRVSFADNQG
LALTMVKVFSEFDDPLDMPFNITELLDNIVSLTTAESESFVLDFSQPSADYLDFRNRLQADHVCLENCVL
KDKAIACTVKVQNLAFEKTVKIRMTFDTWKSYPDPCQYVKDTYAGSDRDTFSFDISLPEKIQSYERMEF
AVYYECNGQTYWDSNRGKNYRIIRAELKSTQGMTKPHSGPDLGISFDQFGSPRCSYGLFPEWPSYLGYEK
LGPYY**

FIG. 28

Score = 3195 (479.4 bits), Expect = 2.8e-138, P = 2.8e-138
Identities = 763/903 (84%), Positives = 763/903 (84%), Strand = Plus / Plus

```

Query:      6 AGGGTTCTAGCCTGTTTCATCTAGCCCCATGATGGCTGTGGACATCGAGTACAGATACAAC 65
            AG TTCTAGCCTG C TCTA C   TGATGGC GTGGACAT GA TACAG TACA C
Sbjct:     65 AGACTTCTAGCCTGCCCTCTAACG---TGATGGCCGTGGACATAGAATACAGCTACAGC 121

Query:     66 TGCATGGCTCCTTCTCTGCGCCAAGAGAGGTTTGCCTTTAAGATCTCACAAAGCCCAGC 125
            G ATGGC CCTTC TCGGC AGAG G TT CCTT AAGATCTC CC AA C A C
Sbjct:    122 AGTATGGCCCCCTTCTCTGCGCAGAGAGCGCTTCACCTTCAAGATCTCCCCCAAACCTGAAC 181

Query:    126 AAACCACTGAGGCCCTTGTATTTCAGCTGAGCAGCAAGAATGAAGCCAGTGAATGGTGGCC 185
            AA CCACTGAGGCCCTTGTATTTCAGCTG GCAGCAAG ATGAAGCC G GAATGGTGGCC
Sbjct:    182 AAGCCACTGAGGCCCTTGTATTTCAGCTGGGCAGCAAGGATGAAGCCGGCAGAATGGTGGCC 241

Query:    186 CCGCTGTCCAGGAGAAGAAGGTGAAAAAGCGGGTGTCTTCGCAGACAACCAGGGGCTG 245
            CC C GT CAGGAGAAGAAGGTGAA AAGCGGGTGTCTTCGC GACAACCAGGGGCTG
Sbjct:    242 CCCACAGTACAGGAGAAGAAGGTGAAGAAGCGGGTGTCTTCGCCGACAACCAGGGGCTG 301

Query:    246 GCCCTGACAAATGGTCAAAGTGTCTCGGAATTCGATGACCCGCTAGATATGCCATTCAAC 305
            GCCCT ACAATGGT AAAGTGTCTTCGGAATTCGATGACCC CTAGATAT CC TT AAC
Sbjct:    302 GCCCTAACAAATGGTCAAAGTGTCTCGGAATTCGATGACCCACTAGATATTCCGTTTAAAC 361

Query:    306 ATCACCGAGCTCCTAGACAACATTGTGAGCTTGACGACAGCAGAGAGCGAGAGCTTTGTT 365
            ATCAC GAGCTCCTAGACAACAT GTGAG TGACGACAGCAGAGAG GAGAGCTTTGTT
Sbjct:    362 ATCACTGAGCTCCTAGACAACATCGTGAGTCTGACGACAGCAGAGAGTGAAGCTTTGTT 421

Query:    366 CTGGATTTTTCAGCCCTCTGCAGATTACTTAGACTTTAGAAATCGACTTCAGGCCGAC 425
            TGGATTTT C CAGCC TCTGCAGATTACTTAGACTTTAGAAATCG CTTCAG CC AC
Sbjct:    422 TTGGATTTTTCAGCCCTCTGCAGATTACTTAGACTTTAGAAATCGGCTTCAGACCAAC 481

Query:    426 CACGTCGTCCCTTGAGAACTGTGTGCTCAAGGACAAGGCCATTGACGGCACTGTGAAGGTT 485
            CA GTCTGCCT GA AACTG GTGCT AAGGA AA GCCAT GC GGCAC GT AAGGT
Sbjct:    482 CATGTCGTCCCTCGAAAACGTGCTGCTGAAGGAGAAGCCATCGCGGCACCGTCAAGGTC 541

Query:    486 CAGAACCTCGCATTTGAGAAGACCGTGAAAAATAAGGATGACGTTGACACCTGGAAGAGC 545
            CAGAACCT GCATT GAGAAG GTGAA AT AG ATGAC TTCA ACCTGGAA AGC
Sbjct:    542 CAGAACCTGGCATTCGAGAAGGTTGTGAAGATCAGCATGACATTGATACCTGGAAAAGC 601

Query:    546 TACACAGACTTTCTTGTGTCAGTACGTGAAGGACACTTATGCCGGTTTCAGACAGGGACACG 605
            T CACAGACTT CCTTGTGTCAGT GTGAAGGACACTTA GC GGTTCAGACAGGGACAC
Sbjct:    602 TTCACAGACTTCCCTTGTGTCAGTATGTGAAGGACACTTACGCTGGTTTCAGACAGGGACACA 661

Query:    606 TTCTCCTTCGACATCAGCTTGCCCCGAGAAGATTTCAGTCTTATGAAAGAATGGAGTTTGCT 665
            TTCTCCTT GA ATCAGC T CC GAGAA AT CAGTCTTATGAAAGAATGGAGTT GC
Sbjct:    662 TTCTCCTTGTATATCAGCTACCGGAGAAAATCCAGTCTTATGAAAGAATGGAGTTTCGCC 721

Query:    666 GTGTACTACGAGTGCAATGGACAGACGTAAGGACAGCAACAGAGGCAAGAACTATAGG 725
            GTGT CTACGAGTG AA GG CAG CGTACTGGGACAGCAACA AGGCAA AACTA AGG
Sbjct:    722 GTGTGCTACGAGTGTAACGGCCAGTCGTACTGGGACAGCAACAAAGGCAAAAACCTACAGG 781

Query:    726 ATCATCCGGGCTGAGTTAAATCTACCCAGGGAATGACCAAGCCCCACAGTGGACCGGAT 785
            ATCA C GGGC GA T A ATC ACCCAGGGAATGAC AGCC ACA TGG CCGGAT
Sbjct:    782 ATCACCAGGGCCGAACCTCAGATCCACCCAGGGAATGACTGAGCCGTACAATGGGCCGGAT 841

Query:    786 TTGGGAATATCCTTTGACCAGTTTCGGAAGCCCTCGGTGTTCCTATGGTCTGTTTCCAGAG 845
            TT GGAAT TC TTTGACCAGTTTCG AGCCCTCGGTGTTCCT GG CTGTTTCCAGAG
Sbjct:    842 TTTGGAATCTCTTTTACCAGTTTCGGGAGCCCTCGGTGTTCCTTCGGCCTGTTTCCAGAG 901

Query:    846 TGGCCAAGTTACTTAGGATATGAAAAGCTAGGGCCCTACTACTAGTGA-----CTGCAGG 900
            TGGCC AGTTA T GG TATGAAAAGCT GGGCCCTA TACTAGTGA CTGCAG
Sbjct:    902 TGGCCTAGTTATCTGGGGTATGAAAAGCTGGGGCCCTATTACTAGTGAGTTGACTGCAGT 961

Query:    901 TGACAG 906
            TGACAG
Sbjct:    962 TGACAG 967

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FIG. 29

Score = 1366 (480.9 bits), Expect = 1.3e-139, P = 1.3e-139
Identities = 255/284 (89%), Positives = 270/284 (95%)

Query: 2 MAVDIEYRYNCMAPSLRQERFAFKISPKPSKPLRPCIQLSSKNEASGMVAPVQEKVK 61
MAVDIEY Y+ MAPSLR+ERF FKISPK +KPLRPCIQL SK+EA MVAP VQEKVK
Sbjct: 1 MAVDIEYSYSSMAPSLRRERFTFKISPKLNKPLRPCIQLGSKDEAGRMVAPT VQEKVK 60

Query: 62 RVSFADNQGLALTMVKVFSEFDDPLDMPFNITELLDNIVSLTTAESESFVLDFSQPSADY 121
RVSFADNQGLALTMVKVFSEFDDPLD+PFNITELLDNIVSLTTAESESFVLDF QPSADY
Sbjct: 61 RVSFADNQGLALTMVKVFSEFDDPLDIPFNITELLDNIVSLTTAESESFVLDFPQPSADY 120

Query: 122 LDFRNRLQADHVCLENCVLKDKAIAGTVKVQNLAFETVKIRMTFDTWKS YTDFFPCQYVK 181
LDFRNRLQ +HVCLENCVLK+KAIAGTVKVQNLAFETVKIRMTFDTWKS+TDFPCQYVK
Sbjct: 121 LDFRNRLQTNHVCLENCVLKEKAIAGTVKVQNLAFETVKIRMTFDTWKSFTDFPCQYVK 180

Query: 182 DTYAGSDRDTFSFDISLPEKIQSYERMEFAVYECNGQTYWDSNRGKNYRI IRAELKSTQ 241
DTYAGSDRDTFSFDISLPEKIQSYERMEFAV YECNGQ+YWDSN+GKNYRI RAE L+STQ
Sbjct: 181 DTYAGSDRDTFSFDISLPEKIQSYERMEFAVCYECNGQSYWDSNKGKNYRI ITRAE LRSTQ 240

Query: 242 GMTKPHSGPDIGISFDQFGSPRCSYGLFPEWPSYLGYEKLG PYY 285
GMT+P++GPD GISFDQFGSPRCS+GLFPEWPSYLGYEKLG PYY
Sbjct: 241 GMTPEYNGPDFGISFDQFGSPRCSFGLFPEWPSYLGYEKLG PYY 284

FIG. 30

Based on this alignment, black outlined amino acid residues indicate regions of conserved sequence (i.e., regions that may be required to preserve structural or functional properties); greyed amino acid residues can be mutated to a residue with comparable steric and/or chemical properties without altering protein structure or function (e.g. L to V, I, or M); non-highlighted amino acid residues can potentially be mutated to a much broader extent without altering structure or function.

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Q63759_PP1_RAT      .....MAMDIEYSYSSMPPSLR..RERFTFISPKLNFLMPCYCLG
AC016485_A          .....MAMDIEYRYNCMPSLR..QERAFKISPKPSPLPCCLIS
O08541_PP1_MOUSE    .....MAMRICLAHSFPLKSFLEPYNGFCRNFVNLNPLDQSSV-
AAD33215_PPP1R5_HUMAN MIQVLDRPLTSSVMPVDVLRRECLAHSEPVKSFLEPYNEFCRNFVNLNPLDQSSV-

Q63759_PP1_RAT      SHDEAGRMVAPTVCCKVKKVVSADNQSLALTMKKVFSDFDP..LQMPNNTTELLNI
AC016485_A          SHDEAGSMVAPAVCKVKKVVSADNQSLALTMKKVFSDFDP..LQMPNNTTELLNI
O08541_PP1_MOUSE    -HQEANSQSEWSPHNQAKKRVFADSKSLSLTAHHVFSGLPPEPAWDLQDYLQNLNIS
AAD33215_PPP1R5_HUMAN -SHKAKSQNDWECSHNQAKKRVFADSKSLSLTAHHVFSGLPPEPAWDLQDYLQNLNIS

Q63759_PP1_RAT      VSLTTIAESSEFVLDFPQPSADYLDERRNLDTTHVCLENGVLHMAAAGTVVQHAFAENV
AC016485_A          VSLTTIAESSEFVLDFSPSADYLDERRNLADHVCLENGVLHMAAAGTVVQHAFAENV
O08541_PP1_MOUSE    SSKLHHEEKNLWDFDFPQPSDYLSERDFQRNFVCLENGSEEDTITSTGVVKKMSFEKK
AAD33215_PPP1R5_HUMAN SSKLHHEEKNLWDFDFPQPSDYLSERDFQRNFVCLENGSEEDTITSTGVVKKMSFEKK

Q63759_PP1_RAT      VKLRMTFDTWKSHTDFPQPSADYLDERRNLDTTHVCLENGVLHMAAAGTVVQHAFAENV
AC016485_A          VKLRMTFDTWKSHTDFPQPSADYLDERRNLDTTHVCLENGVLHMAAAGTVVQHAFAENV
O08541_PP1_MOUSE    VQARRTFDTWKSHTDFPQPSADYLDERRNLDTTHVCLENGVLHMAAAGTVVQHAFAENV
AAD33215_PPP1R5_HUMAN VQARRTFDTWKSHTDFPQPSADYLDERRNLDTTHVCLENGVLHMAAAGTVVQHAFAENV

Q63759_PP1_RAT      SYWDSKKEKNYRITRAELR..STGMIETYN.....EDFGISDFDQFGSPSCSYDLFPE
AC016485_A          SYWDSKKEKNYRITRAELR..STGMIETYN.....EDFGISDFDQFGSPSCSYDLFPE
O08541_PP1_MOUSE    IYWDNNEGQNYRIVHVQWPEGVETQVARKDCARQGPKEIEPTVFGSPRLASGLFPE
AAD33215_PPP1R5_HUMAN VYWDNNDGQNYRIVHVQWPEGVETQVARKDCARQGPKEIEPTVFGSPRLASGLFPE

Q63759_PP1_RAT      WPSGLGYEKLGPY
AC016485_A          WPSGLGYEKLGPY
O08541_PP1_MOUSE    WPSGRVENLTSR
AAD33215_PPP1R5_HUMAN WPSGRMENLTSR

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FIG. 31

CTGTCTCCTGCATTCTCCTGAAACCTTCATCCACACAATGCCTCCCAACCTCACTGGC
TACTACCGCTTTGTCTCGCAGAAGAACATGGAGGACTACCTGCAAGCCCTAAACATC
AGCTTGGCTGTGCGGAAGATCGCGCTGCTGCTGAAGCCGGACAAGGAGATCGAACA
CCAGGGCAACCACATGACGGTGAGGACGCTCAGCACCTTCCGAAACTACACTGTGC
AGTTTGATGTGGGAGTGGAGTTTGAGGAGGACCTCAGGAGCGTGGACGGACGAAAA
TGCCAGATCTCATTCGTTCGGTTCGGATCCAAGCCAGTTCTGTGGTCAGCAAGGCTCC
CCTCTGGGCAGGCCCCCTGGTCAGAGGGAGTTTGTATCCTCAGGGAGGAGTTTGCGG
CTGACCTTCCGCACACAGCCTTCCTCGGAGAACAAAGACTGCCCACCTCCACAAGGGC
TTCTGGCCCTCTACCAAACCGTGGCCTTAAGTGGAAGCTTGAGTGACAGCTGAGGC
TGGGGACTCAGGGACACCTGGGCTGGATCCCAGCCCTGCC

FIG. 32

**MPPNLTGYR FVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFR
NYTVQFDVGVEFEEDLRSVDGRKCQISFVGSDPSQFCGQQGSPLGRPPGQREFVSSGRSL
RLTFRTQPSSSENKTAHLHKGFLALYQTVALSGLSDS**

FIG. 33

Score = 355 (125.0 bits), Expect = 1.0e-31, P = 1.0e-31
Identities = 68/70 (97%), Positives = 70/70 (100%), Frame = +2

Query: 38 MPPNLTGYRPFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN 217
MPPNLTGYRPFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN
Sbjct: 1 MPPNLTGYRPFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN 60

Query: 218 YTVQFDVGVE 247
YT+QFDVGV+
Sbjct: 61 YTLQFDVGVSQ 70

FIG. 34

CTGTCTCCTGCATTCTCCTGAAACCTTCATCCACACAATGCCTCCCAACCTCACTGGCTACTACCGCTTT
GTCTCGCAGAAGAACATGGAGGACTACCTGCAAGCCCTAAACATCAGCTTGGCTGTGCGGAAGATCGCGC
TGCTGCTGAAGCCGGACAAGGAGATCGAACACCAGGGCAACCACATGACGGTGAGGACGCTCAGCACCTT
CCGAAACTACACTGTGCAGTTTGATGTGGGAGTGGAGTTTGAGGAGGACCTCAGGAGCGTGGACGGACGA
AAATGCCAGACCATAGTAACCTGGGAGGAGGAGCACCTGGTGTGTGTGCAGAAAGGGGAGGTCCCCAACC
GGGGCTGGAGACACTGGCTGGAGGGAGAGTTGCTGTATCTGGAAGTGAAGGATGCAAGGGATGCAGTGTGCGA
GCAGGTCTTCAGGAAGGTCAGATAGCCGGAGAGGAGCCAAGATCCCTCCAGACAGCACCAGCTCACAGAC
GCTCTTGTTGTGCCCCCTTCAAGCCCAGATTGTGCCAGATCTCATTCTCGTTCGGTTCGGATCCAAGCCAGTT
CTGTGGTCAGCAAGGCTCCCCCTCTGGGCAGGCCCCCTGGTCAGAGGGAGTTTGTATCCTCAGGGAGGAGT
TTGCGGCTGACCTTCCGCACACAGCCTTCCTCGGAGAACAAGACTGCCCACCTCCACAAGGGCTTCCTGG
CCCTCTACCAAACCGTGGGTGAGTGTCCCTCCTGGGGGTGCAGGGAGGGAGCCTCTGTTCACAGCCATGA
CCCTGGTATCTTCAAGCCTTAAGTGGAAGCTTGAGTGACAGCTGAGG

FIG. 35

MPPNLTGYRFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRNYTVQFDVGVE
FEEDLRSVDGRKCQTIVTWEEHLVCVQKGEVPNRGWRHWLEGELLYLELTARDAVCEQVFRKVR

FIG. 36

Score = 712 (250.6 bits), Expect = 1.5e-69, P = 1.5e-69
Identities = 133/135 (98%), Positives = 135/135 (100%), Frame =
+2

Query: 38 MPPNLTGYRPFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN 217
MPPNLTGYRPFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN
Sbjct: 1 MPPNLTGYRPFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN 60

Query: 218 YTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEHLVCVQKGEVPNRGWRHWLEGEMLYLEL 397
YT+QFDVGVEFEEDLRSVDGRKCQTIVTWEEHLVCVQKGEVPNRGWRHWLEGE+LYLEL
Sbjct: 61 YTLQFDVGVEFEEDLRSVDGRKCQTIVTWEEHLVCVQKGEVPNRGWRHWLEGEMLYLEL 120

Query: 398 TARDAVCEQVFRKVR 442
TARDAVCEQVFRKVR
Sbjct: 121 TARDAVCEQVFRKVR 135

FIG. 37

C018653_A MPPNLTGYVRFVSOQNMEDYLQALNISLAVKIALLLKPDKEIEHOCNHMTVRTLSTFRN
C018653_dal_ MPPNLTGYVRFVSOQNMEDYLQALNISLAVKIALLLKPDKEIEHOCNHMTVRTLSTFRN

C018653_A YTVCFDVGVEFEEDLRSVDRHCCISFVGSPSQFSGQSPLOPPCQREFVRSR
C018653_dal_ YTVCFDVGVEFEEDLRSVDRHCCITVTWEEHLVVKKEVPNE--LWEHHE-DEELY

C018653_A LTFRTQPSSSENKTAHLHGFLLALYOTVALSGSLSDS
C018653_dal_ LELTARDAVCEQVFRKV-----